

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 13:56:56 ; Search time 21 Seconds
(without alignments)
18.318 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20
Sequence: 1 VLEP 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	28	2	A27261
2	20	100.0	37	2	G28027
3	20	100.0	58	2	S03810
4	20	100.0	59	2	B60232
5	20	100.0	59	2	AC3286
6	20	100.0	61	2	T03065
7	20	100.0	62	2	C90471
8	20	100.0	63	2	E89802
9	20	100.0	68	2	G84484
10	20	100.0	77	2	C72645
11	20	100.0	80	2	T15286
12	20	100.0	81	2	E90324
13	20	100.0	82	2	T42003
14	20	100.0	83	2	T19717
15	20	100.0	86	2	C69107
16	20	100.0	89	2	B72296
17	20	100.0	92	2	JN0349
18	20	100.0	93	2	B86755
19	20	100.0	93	2	B91217
20	20	100.0	93	2	F86063
21	20	100.0	93	2	S48658
22	20	100.0	93	2	AE0923
23	20	100.0	99	2	T37093
24	20	100.0	101	2	T25556
25	20	100.0	102	2	S52711
26	20	100.0	103	2	E86564
27	20	100.0	103	2	H72060
28	20	100.0	105	1	R6MXER
29	20	100.0	105	2	S04150

30	20	100.0	105	2	AE1848	hypothetical prote
31	20	100.0	105	2	S76770	hypothetical prote
32	20	100.0	106	2	E81606	conserved hypothet
33	20	100.0	108	2	T13133	protein gp46 - pha
34	20	100.0	108	2	T41447	very hypothetical
35	20	100.0	109	2	B70637	hypothetical prote
36	20	100.0	111	2	D72112	hypothetical prote
37	20	100.0	111	2	F86511	hypothetical prote
38	20	100.0	112	2	B69438	hypothetical prote
39	20	100.0	113	2	T30436	hypothetical prote
40	20	100.0	113	2	F90319	hypothetical prote
41	20	100.0	114	2	H87313	nitrogen regulator
42	20	100.0	115	2	F72716	hypothetical prote
43	20	100.0	115	2	G83426	hypothetical prote
44	20	100.0	116	1	Q0RSHT	hypothetical prote
45	20	100.0	116	1	Q0EBHT	hypothetical prote

ALIGNMENTS

RESULT 1
A27261
proteinnase inhibitor 3 - sea anemone (Stichodactyla sp.) (fragments)
C/Species: Stichodactyla sp., Stichodactis sp.
C/Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1993
C/Accession: A27261
R/Refs: D.; Gebauer, E.
Toxinon 20, 335, 1982
A/Title: Structural studies on a proteinnase inhibitor from the sea anemone Stichodactis ;
A/Reference number: A27261
A/Accession: A27261
A/Molecule type: protein
A/Residues: 1-28 <MB>

Query Match 100.0%; Score 20; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
|||||
Db 4 VLEP 7

RESULT 2
G28027
protein p10 - curled-leaved tobacco (fragment)
C/Species: Nicotiana glauca (curled-leaved tobacco)
C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 11-Jan-2000
C/Accession: G28027
R/Baum, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A/Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid.
A/Reference number: A94167
A/Accession: G28027
A/Molecule type: protein
A/Residues: 1-37 <80>
C/Superfamily: thaumatin I

Query Match 100.0%; Score 20; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1,1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
|||||
Db 29 VLEP 32

RESULT 3
S03810
psal protein - Rhizobium leguminosarum bv. phaseoli
C/Species: Rhizobium leguminosarum bv. phaseoli
C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 11-Jan-2000

C/Accession: S03810
R:Borthakur, D.; Barker, R.F.; Latchford, J.W.; Roessen, L.; Johnston, A.W.B.
Mol. Gen. Genet. 213: 155-162, 1998
A/Title: Analysis of pse genes of Rhizobium leguminosarum required for exopolysaccharide genes.

A/Reference number: S03810; MUID:89127136; PMID:2851702

A/Accession: S03810

A/Molecule type: DNA

A/Residues: 1-58 <BOR>

A/Cross-references: EMBL:X12568; NID:g46255; PIDN:CAJ1078.1; PID:g46256

C/Genetics:

A/Status: psl

C/Superfamily: Aquifex aeolicus cysQ protein

Query Match 100.0%; Score 20; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
|||
DB 54 VLEP 57

RESULT 4

B60232 T-cell surface glycoprotein CD3 delta chain precursor - bovine (fragment)

C/Species: Bos primigenius taurus (cattle)

C/Date: 08-Dec-1992 #sequence_revision 08-Dec-1992 #text_change 23-Jul-1999

C/Accession: B60232

R/Clevers, H.; MacHugh, N.D.; Benaïd, A.; Dunlap, S.; Baldwin, C.L.; Kaushal, A.; Iams,

Eur. J. Immunol. 20, 809-817, 1990

A/Title: Identification of a bovine surface antigen uniquely expressed on CD4-CD8- T cell

A/Reference number: A60232; MUID:90265333; PMID:1971793

A/Accession: B60232

A/Molecule type: mRNA

A/Residues: 1-59 <CLE>

A/Cross-references: GB:X53269; NID:g287745; PIDN:CAJ3767.1; PID:g287746

C/Superfamily: T-cell surface glycoprotein CD3 delta chain; immunoglobulin homology

C/Keywords: glycoprotein; receptor; T-cell; transmembrane protein

Query Match 100.0%; Score 20; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
|||
DB 26 VLEP 29

RESULT 5

AC3286 LSU ribosomal protein L32P [imported] - Brucella melitensis (strain 16M)

C/Species: Brucella melitensis

C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 17-May-2002

C/Accession: AC3286

R/Delvecchio, V.G.; Kapellat, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova,

; Mazur, M.; Goldsman, B.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes,

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A/Reference number: AD3252; PMID:11756688

A/Accession: AC3286

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-59 <KUR>

A/Cross-references: GB:AE008917; PIDN:AL51454.1; PID:g17982164; GSPDB:GN00190

C/Genetics:

A/Status: BMF0272

A/Map position: I

C/Superfamily: Escherichia coli ribosomal protein L32

Query Match 100.0%; Score 20; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLEP 4
|||
DB 54 VLEP 57

RESULT 6

T03065 Cytochrome-c oxidase homolog 043L - Chilo iridescent virus

C/Species: Chilo iridescent virus

C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999

C/Accession: T03065

R/Bahr, U.; Tidona, C.A.; Darai, G.

Virus Genes 15, 235-245, 1997

A/Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101

A/Reference number: Z14834; MUID:98141693; PMID:9482589

A/Accession: T03065

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-61 <BAH>

A/Cross-references: EMBL:AF005534; NID:g2738385; PIDN:AA94439.1; PID:g2738412

Query Match 100.0%; Score 20; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
|||
DB 53 VLEP 56

RESULT 7

C90471 Hypothetical protein SSO11456 [imported] - Sulfolobus solfataricus transposon ISCI058

C/Species: Sulfolobus solfataricus

C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001

C/Accession: C90471

R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan

Jong, I.; Jellies, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,

arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.

Submitted to Genbank, April 2001

A/Description: Sulfolobus solfataricus complete genome.

A/Reference number: A99139

A/Accession: C90471

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-62 <KUR>

A/Cross-references: GB:AE006641; NID:g13816289; PIDN:AAK43026.1; GSPDB:GN00155

C/Genetics:

Query Match 100.0%; Score 20; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
|||
DB 20 VLEP 23

RESULT 8

E89802 Hypothetical protein [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C/Accession: E89802

R/Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu

ma, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;

C.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: AB9758; MUID:21311952; PMID:11418146

A:Accession: E89802
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-63 <KUR>
A:Cross-references: GB:BA000018; PID:g13700278; PIDN:BA841576.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SAS009

Query Match 100.0%; Score 20; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 35 VLEP 38

RESULT 9
G84484
hypothetical protein AC2907350 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: G84484
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentol, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Neus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: AB4420; MUID:20083487; PMID:10617197

A:Accession: G84484
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-68 <STO>
A:Cross-references: GB:AE002093; NID:G4309758; PIDN:AAD15527.1; GSPDB:GN00139
C:Genetics:
A:Gene: AC2907350
A:Map position: 2

Query Match 100.0%; Score 20; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 6 VLEP 9

RESULT 10
C72645
hypothetical protein APE0025 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: C72645
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatakawa, Y.; Jin-no, K.; Takahara, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
A:Reference number: A72450; MUID:9310339; PMID:10382966

A:Accession: C72645
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-77 <KAM>
A:Cross-references: DDBJ:AP000060; NID:G5104188; PIDN:BA479563.1; PID:d1043349; PID:G510
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0025

Query Match 100.0%; Score 20; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4

DB 30 VLEP 33

RESULT 11
T15286
hypothetical protein M01D7.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15286
R:Gatung, S.; Goela, D.; Wilson, R.

A:Title: The sequence of C. elegans cosmid M01D7.
A:Description: Submitted to the EMBL Data Library, May 1997

A:Reference number: Z18322
A:Accession: T15286
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-80 <GAT>
A:Cross-references: EMBL:AF003739; NID:G2105482; PID:G2105484; PIDN:AAB58066.1; GSPDB:G
A:Experimental source: strain Bristol N2; clone M01D7
C:Genetics:
A:Gene: CRSP.M01D7.5
A:Map position: 1
A:Introns: 19/1; 38/3

Query Match 100.0%; Score 20; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 72 VLEP 75

RESULT 12
E90324
hypothetical protein SS08568 [imported] - Sulfolobus solfataricus transposon ISCT1229
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: E90324
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweez, M.J.; Chan
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, J.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: E90324
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-81 <KUR>
A:Cross-references: GB:AE006641; NID:g13814884; PIDN:AAK1852.1; GSPDB:GN00155
C:Genetics:
A:Gene: SS08568

Query Match 100.0%; Score 20; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 23 VLEP 26

RESULT 13
T42003
hypothetical protein H3 - human herpesvirus 7 (strain J1)

C:Species: human herpesvirus 7
A:Variety: strain J1
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
C:Accession: T42003
R:Nicholas, J.
submitted to the EMBL Data Library, December 1995
A:Description: Determination and analysis of the complete nucleotide sequence of human 1

A:Reference number: Z22022
 A:Accession: T41904
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-82 <NT>
 A:Cross-references: EMBL:U43400; PIDN:AAC54664.1
 A:Experimental source: strain J1
 A:Genetics: GN1
 A:Accession: T42003
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-82 <NT>
 A:Cross-references: EMBL:U43400; PIDN:AAC54763.1
 A:Experimental source: strain J1
 A:Genetics: GN2
 A:Gene: H3
 A:Map position: 3976-4224
 A:Genetics: <GN2>
 A:Gene: H3
 A:Map position: 143023-143271

Query Match 100.0%; Score 20; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
 ||||
 Db 19 VLEP 22

RESULT 14
 T41917
 hypothetical protein C34D1.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T19717
 R:Baynes, C.
 submitted to the EMBL Data Library, August 1996
 A:Reference number: Z19168
 A:Accession: T19717
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-83 <MTL>
 A:Cross-references: EMBL:Z78060; PIDN:CAB01491.1; GSPDB:GN00023; CESP:C34D1.1
 A:Experimental source: clone C34D1
 C:Genetics: C
 A:Gene: CESP:C34D1.1
 A:Map position: 5
 A:Introns: 35/1; 57/2

Query Match 100.0%; Score 20; DB 2; Length 83;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
 ||||
 Db 25 VLEP 28

RESULT 15
 C69107
 hypothetical protein MTH1799 - Methanobacterium thermoautotrophicum (strain Delta H)
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C:Accession: C69107
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 ; Qu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
 K.; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
 A:Reference number: A69000; MUID:98037514; PMID:9371463
 A:Accession: C69107

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-86 <MTH>
 A:Cross-references: GB:AE000934; GB:AE000666; NID:g2622924; PIDN:ABB6265.1; PID:g26229
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH1799

Query Match 100.0%; Score 20; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
 ||||
 Db 58 VLEP 61

Search completed: November 25, 2003, 14:00:52
 Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 13:47:36 ; Search time 11 Seconds

(Without alignments)
17.101 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20
Sequence: 1 VLEP 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	59	1 CD3D_BOVIN	Q28072 bos laurus
2	20	100.0	59	1 RL32_BRUME	Q8y132 bruceella me
3	20	100.0	71	1 IPI1_LEPIN	Q9xd14 leprospira
4	20	100.0	92	1 PPI1_ECOLI	P39159 escherichia
5	20	100.0	92	1 PPI1_SATY	Q91683 salmonella
6	20	100.0	95	1 YPS1_RHLP	P10497 rhizobium 1
7	20	100.0	98	1 RPO2_THAQ	Q9evv4 thermus aqu
8	20	100.0	99	1 RPO2_THAQ	Q8rgq7 thermus the
9	20	100.0	100	1 VG6_BPB03	Q37886 bacterioph
10	20	100.0	103	1 V592_CHLPN	Q92782 chlamydia p
11	20	100.0	105	1 RL32_MERVA	P14025 methanococ
12	20	100.0	106	1 PETD_HOKVU	P12361 hordeum vul
13	20	100.0	112	1 YF07_ARCFU	Q28765 archaeoglob
14	20	100.0	114	1 RL32_EIMTE	Q96799 eimeria ten
15	20	100.0	116	1 MERT_ACICA	Q52106 acinetobact
16	20	100.0	116	1 MERT_ALCSP	P94185 alcaligenes
17	20	100.0	116	1 MERT_PSEAE	P04180 pseudomonas
18	20	100.0	116	1 MERT_PSEFL	Q51769 pseudomonas
19	20	100.0	116	1 MERT_SALTI	P04336 salmonella
20	20	100.0	116	1 MERT_SERMA	P13112 serratia ma
21	20	100.0	116	1 REV_HVIOY	P20887 human immun
22	20	100.0	117	1 DHSD_ARCFU	Q29573 archaeoglob
23	20	100.0	120	1 SYE_STAXY	P77984 staphylococ
24	20	100.0	126	1 MERT_ENTAG	P94700 enterobacte
25	20	100.0	129	1 UMP1_SCHPO	Q74416 schizosacch
26	20	100.0	129	1 YIO1_YEAST	P40461 saccharomyc
27	20	100.0	134	1 NNT1_CHICK	Q91029 gallus gall
28	20	100.0	136	1 RK16_MATZE	P08528 zea mays (m
29	20	100.0	139	1 PETD_PEA	P06527 pisum sativ
30	20	100.0	146	1 YN81_YEAST	P40342 saccharomyc
31	20	100.0	147	1 VG36_HSV1	Q00146 icatalturid h
32	20	100.0	150	1 ZFP2_ARATH	Q39261 arabidopsis
33	20	100.0	153	1 IEX1_MOUSE	P46694 mus musculu

34	20	100.0	156	1 IEX1_HUMAN	P46695 homo sapien
35	20	100.0	157	1 HES2_MOUSE	Q54792 mus musculu
36	20	100.0	157	1 HES2_RAT	P35429 ratu mus norv
37	20	100.0	158	1 WH21_MYXVL	P28850 myxoma viru
38	20	100.0	160	1 PETD_ARATH	P56774 arabidopsis
39	20	100.0	160	1 PETD_LOTJA	Q9bq5 lotus japon
40	20	100.0	160	1 PETD_MAIZE	P05643 zea mays (m
41	20	100.0	160	1 PETD_MARPO	P06250 marchantia
42	20	100.0	160	1 PETD_MESVI	Q9muv2 mesostigma
43	20	100.0	160	1 PETD_ORYSA	P12118 oryza sativ
44	20	100.0	160	1 PETD_SPIOL	P00166 spinacia ol
45	20	100.0	160	1 PETD_TOBAC	P06249 nicotiana t

ALIGNMENTS

RESULT 1
CD3D_BOVIN STANDARD; PRT; 59 AA.
ID CD3D_BOVIN
AC Q28072;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE T-cell surface glycoprotein CD3 delta chain precursor (T-cell receptor
DE T3 delta chain) (Fragment).
GN CD3D.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=90269333; PubMed=1971793;
RA Klevers H., Machugh N.D., Bensaïd A., Dunlap S., Baldwin C.L.,
RA Kaushal A., Jams K., Howard C.J., Morrison W.I.;
RT "Identification of a bovine surface antigen uniquely expressed on
RT CD4-CD8-T cell receptor gamma/delta+ T lymphocytes.";
RL Eur. J. Immunol. 20:809-817(1990).
CC -1- FUNCTION: THE CD3 COMPLEX MEDIATES SIGNAL TRANSDUCTION.
CC -1- SUBUNIT: THE TCR/CD3 COMPLEX OF T LYMPHOCYTES CONSISTS OF EITHER
CC A TCR ALPHA/BETA OR TCR GAMMA/DELTA HETERODIMER COEXPRESSED AT THE
CC CELL SURFACE WITH THE INVARIANT SUBUNITS OF CD3 LABELED GAMMA,
CC DELTA, EPSILON, ZETA, AND ETA.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
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DR EMBL: X53269; CAA37367.1; -
DR PIR: B60232; B60232.
KW T-cell; Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 >59
FT DOMAIN 22 >59
FT CARBHYD 38 38
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6468 MW; DE2C50A9C99F40E CRC64;
Query Match 100.0%; Score 20; DB 1; Length 59;
Best local similarity 100.0%; Pred. No. 73;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLEP 4
Db 26 VLEP 29

RESULT 2

RL32_BRUME STANDARD; PRT; 59 AA.
 ID RL32_BRUME
 AC OEYJ14;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 50S ribosomal protein L32.
 GN RPF OR BME10272 OR BR1775.
 OS Brucella melitensis, and
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella
 NCBI_TaxID=29459, 29461;
 OX (1)
 RP SEQUENCE FROM N.A.
 RC SPECIES=B.melitensis; STRAIN=16M / ATCC 23456 / Biotype 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA Delvecchio V.G., Kaparatel V., Redkar R.J., Patra G., Mujer C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
 RA Ushlonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
 RA Seltkov E., Elzer P.H., Hagius S., O'Callaghan D., Leveson J.-J.,
 RA Haselkorn R., Kyriades N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=B.suis; STRAIN=1330 / Biovar 1;
 RX MEDLINE=22247741; PubMed=12271122;
 RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 RA Read T.D., Dodson R.J., Unayen L., Brinkac L.M., Beanan M.J.,
 RA Daugherty S.C., Debey R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Ayodeji B., Krahl M., Shetty J., Malek J., Van Aken S.E.,
 RA Riedmiller S., Tectelijn H., Gill S.R., White O., Salzberg S.L.,
 RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
 RT "The Brucella suis genome reveals fundamental similarities between
 RT animal and plant pathogens and symbionts";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
 CC -1- SIMILARITY: BELONGS TO THE L32P FAMILY OF RIBOSOMAL PROTEINS.
 CC
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 CC
 CC
 DR EMBL; AE009470; AA151454.1; -
 DR EMBL; AE014468; AA030673.1; -
 DR PIR; AC3286; AC3286.
 DR TIGR; BR1775; -
 DR HAMAP; MF_00340; -; 1.
 DR InterPro; IPR002677; Ribosomal_L32P.
 DR InterPro; IPR005718; S12_Dact_Org.
 DR Pfam; PF01783; Ribosomal_L32P; 1.
 DR TIGRPFAM; TIGR01031; rpf_bact; 1.
 KM Ribosomal protein; Complete proteome.
 SQ SEQUENCE 59 AA; 6790 MW; CE3BC2B67F7DF6DB CRC64;

Query Match 100.0%; Score 20; DB 1; Length 59;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
 DB 54 VLEP 57

RESULT 3

IF1 LEPTIN STANDARD; PRT; 71 AA.

ID IF1 LEPTIN
 AC 09XD14;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Translation initiation factor IF-1.
 GN INFA OR LA0761.
 OS Leptospira interrogans.
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 NCBI_TaxID=173;
 OX (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Jai / Serogroup Icterohaemorrhagiae / Serovar Jai;
 RX MEDLINE=20088935; PubMed=10620683;
 RA Zuercher R.L., Hartskeerl R.A., van de Kemp H., Bal A.E.;
 RT "Characterization of the Leptospira interrogans S10-spc-alpha
 RT operon";
 RL FEMS Microbiol. Lett. 182:303-308(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=56501 / Serogroup Icterohaemorrhagiae / Serovar Jai;
 RX MEDLINE=2258143; PubMed=12712204;
 RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
 RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
 RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
 RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
 RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
 RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
 RA Xu J.-G., Zhao G.-P.;
 RT "Unique physiological and pathogenic features of Leptospira
 RT interrogans revealed by whole-genome sequencing";
 RL Nature 422:888-893(2003).
 CC -1- FUNCTION: No specific function has so far been attributed to this
 CC initiation factor; however, it seems to stimulate more or less all
 CC the activities of the other two initiation factors, IF-2 and IF-3.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the IF-1 family.
 CC -1- SIMILARITY: Contains 1 S1-like domain.
 CC
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 CC
 CC
 DR EMBL; AF115283; AAD40605.1; -
 DR EMBL; AE011862; AA047960.1; -
 DR HSSP; P02998; IAH9.
 DR HAMAP; MF_00075; -; 1.
 DR InterPro; IPR003029; S1.
 DR InterPro; IPR006196; S1_IF1.
 DR InterPro; IPR004368; TIF_IF1.
 DR Pfam; PF00575; S1; 1.
 DR SMART; SM00316; S1; 1.
 DR TIGRPFAM; TIGR00008; infa_1.
 DR PROSITE; PSS0832; S1_IF1-TYPE; 1.
 DR POSITIVE; PSS0832; S1_IF1-TYPE; 1.
 KM Initiation factor; Protein biosynthesis; Complete proteome.
 FT INIT MET 0
 FT DOMAIN 1 71
 FT S1-LIKE
 SQ SEQUENCE 71 AA; 8062 MW; 978564AB12140CD9 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 71;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
 DB 12 VLEP 15

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RESULT 4
P1C1_ECOLI STANDARD; PRT; 92 AA.
AC P39159;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Peptidyl-prolyl cis-trans isomerase C (EC 5.2.1.8) (PPIase C)
DE (Rotamase C) (Parvulin).
GN PIC OR PARVA OR B3775 OR C4697 OR Z5286 OR ECS4709.
OS Escherichia coli O6, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 217992, 83334;
RN
RP SEQUENCE FROM N.A., AND SEQUENCE.
RX MEDLINE=95010704; PubMed=7925971;
RA Rahfeld J.-U., Ruecknagel K.P., Schelbert B., Ludwig B., Hacker J.,
RA Mann K., Fischer G.;
RT "Confirmation of the existence of a third family among
RT peptidyl-prolyl cis/trans isomerases. Amino acid sequence and
RT recombinant production of parvulin.";
RL FEBS Lett. 352:180-184(1994).
RN
RP PRELIMINARY SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=92358234; PubMed=1379743;
RA Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
RT "Analysis of the Escherichia coli genome: DNA sequence of the region
RT from 84.5 to 86.5 minutes.";
RL Science 257:771-778(1992).
RN
RP REVISIONS, AND IDENTIFICATION.
RX MEDLINE=95184297; PubMed=878732;
RA Rudd K.E., Sofia H.J., Koonin E.V., Plunkett G. III, Lazar S.,
RA Rouviere P.E.;
RT "Conserved sequence motifs in bacterial and bacteriophage
RT chaparons.";
RL Trends Biochem. Sci. 20:14-15(1995).
RN
RP SEQUENCE FROM N.A.
RX STRAIN=06:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liu S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
RN
RP SEQUENCE FROM N.A.
RX STRAIN=0157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodoca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohemorrhagic Escherichia coli O157:H7.";
RL Nature 409:329-333(2001).
RN
RP SEQUENCE FROM N.A.
RX STRAIN=0157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli

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RT 0157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN
RP SEQUENCE OF 1-21, AND CHARACTERIZATION.
RX MEDLINE=94215709; PubMed=8163020;
RA Rahfeld J.-U., Scherhorn A., Mann K., Fischer G.;
RT "A novel peptidyl-prolyl cis/trans isomerase from Escherichia coli.";
RL FEBS Lett. 343:65-69(1994).
RN
RP FUNCTION: PIPASES ACCELERATE THE FOLDING OF PROTEINS. IT PREFERS
RN AMINO ACID RESIDUES WITH HYDROPHOBIC SIDE CHAINS LIKE LEUCINE AND
RN PHENYLALANINE IN THE P1 POSITION OF THE PEPTIDE SUBSTRATES.
RN
RN -1- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
RN (omega=0).
RN
RN -1- SUBCELLULAR LOCATION: Cytoplasmic.
RN
RN -1- SIMILARITY: BELONGS TO THE P1C1/PARVULIN FAMILY OF ROTAMASES.
RN
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RN
RN -----
RN EMBL: S73874; AAC32054.1; -
RN EMBL: M87049; AA6578.1; -
RN EMBL: AE000454; AAC76780.1; -
RN EMBL: AE016769; AA083129.1; -
RN EMBL: AE005609; AAG58970.1; -
RN EMBL: AP002566; BAB38132.1; -
RN PIR: E91217; E91217.
RN PIR: F86063; F86063.
RN PIR: S48658; S48658.
RN HSP: Q13526; IPIN.
RN EcoGene: EG12352; P1C1.
RN InterPro: IPR000297; Rotamase.
RN Pfam: PF00639; Rotamase; 1.
RN PROSITE: PS01096; P1C1_PPIASE_1; 1.
RN PROSITE: PS01098; P1C1_PPIASE_2; 1.
RN KX Isomerase; Rotamase; Complete proteome.
RN INIT MET 0
RN SQ SEQUENCE 92 AA; 10101 MW; AE1AE2028277DF4F CRC64;
RN
RN Query Match 100.0%; Score 20; DB 1; Length 92;
RN Best Local Similarity 100.0%; Pred. No. 1,2e+02;
RN Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RN
RN Qy 1 VLEP 4
RN Db 70 VLEP 73
RN
RN RESULT 5
RN P1C1_SALTY STANDARD; PRT; 92 AA.
AC 091653;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Peptidyl-prolyl cis-trans isomerase C (EC 5.2.1.8) (PPIase C)
DE (Rotamase C) (Parvulin).
GN PIC OR STM3910 OR STM01.80 OR STY3647 OR T3388.
OS Salmonella typhimurium, and
OS Salmonella typhimurium, and
OS Salmonella typhimurium, and
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602, 601;
RN
RP SEQUENCE FROM N.A.
RX SPECIES=S. typhimurium, STRAIN=LT2 / SSGC1412 / ATCC 700720;
RX MEDLINE=21334948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Speleth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

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RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Rran E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
RN
RP
RC SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahina M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagsels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gea P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
RN
RP
RC SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=TY2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Lion S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyanni V., Schwartz D.C., Blatner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains TY2
RT and CT18."
RL Bacteriol. 185:2330-2337(2003).
RC
CC -1- FUNCTION: PEPTIDES ACCELERATE THE FOLDING OF PROTEINS. IT PREFERS
CC AMINO ACID RESIDUES WITH HYDROPHOBIC SIDE CHAINS LIKE LEUCINE AND
CC PHENYLALANINE IN THE P1 POSITION OF THE PEPTIDES SUBSTRATES (BY
CC SIMILARITY)
CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PPIC/PARVULIN FAMILY OF ROTAMASES.
CC -----
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CC -----
DR EMBL; AF233324; AAF33475.1; -
DR EMBL; AE008882; AAL22760.1; -
DR EMBL; AL627279; CAD09407.1; -
DR EMBL; AE016845; AAC070912.1; -
DR HSSP; Q13526; 1PIN.
DR ScyGene; SG77777; PPIC.
DR InterPro; IPR000297; Rotamase.
DR Pfam; PF00639; Rotamase; 1.
DR PROSITE; PS01096; PPIC_PP1ASE_1; 1.
DR PROSITE; PS50198; PPIC_PP1ASE_2; 1.
KW isomerase; rotamase; Complete proteome.
FT INIT MET 0 BY SIMILARITY
SQ SEQUENCE 92 AA; 10197 MW; 120263BFB93F924 CRC64;

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AC P10497;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Hypothetical protein in pss 5 region (Fragment).
OS Rhizobium leguminosarum (biovar phaseol1).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=385;
RN [1]
RP
RC SEQUENCE FROM N.A.
RC STRAIN=8002;
RX MEDLINE=89127116; PubMed=2851702;
RA Borthakur D., Barker R.F., Latchford J.W., Rossen L., Johnston A.W.B.;
RT "Analysis of pss genes of Rhizobium leguminosarum required for
RT exopolysaccharide synthesis and nodulation of peas: their primary
RT structure and their interaction with psi and other nodulation
RT genes."
RL Mol. Gen. Genet. 213:155-162(1988).
CC
CC -1- SIMILARITY: Belongs to the inositol monophosphatase family.
CC -----
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DR EMBL; X12568; CAA1078.1; AUL_INIT.
DR InterPro; IPR000760; Inositol_P.
DR Pfam; PF00459; Inositol_P; 1.
DR Prodom; PD023420; Inositol_P; 1.
DR PROSITE; PS00629; IMP_1; PARTIAL.
DR PROSITE; PS00630; IMP_2; 1.
KW Hypothetical protein; Exopolysaccharide synthesis; Nodulation.
FT NON TER 1
SQ SEQUENCE 95 AA; 10149 MW; A3DED04E1BF924B CRC64;

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Query Match 100.0%; Score 20; DB 1; Length 95;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;

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Cy 1 VLEP 4
Db 91 VLEP 94

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RESULT 7
 RPOZ_THEAO STANDARD; PRT; 98 AA.

AC Q9EYV4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE DNA-directed RNA polymerase omega chain (EC 2.7.7.6) (Transcriptase
 DE omega chain) (RNA polymerase omega subunit).
 GN RPOZ.
 OS Thermus aquaticus.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 OX NCBI_TaxID=271;
 RN [1]
 RP
 RC SEQUENCE FROM N.A.
 RC MEDLINE=2056669; PubMed=11114902;
 RA Minakhin L., Nechaev S., Campbell E.A., Severinov K.;
 RT "Recombinant Thermus aquaticus RNA polymerase, a new tool for
 RT structure-based analysis of transcription.";
 RL J. Bacteriol. 183:71-76(2001).
 RN
 RN
 RN
 RP
 RC SEQUENCE FROM N.A., SEQUENCE OF 1-10, FUNCTION, AND 3D-STRUCTURE
 RP MODELING.
 RX MEDLINE=21107642; PubMed=11158566;


```

RA Minakhin L., Bhagat S., Brunning A., Campbell E.A., Darst S.A.,
RA Ebricht R.H., Severinov K.;
RT "Bacterial RNA polymerase subunit omega and eukaryotic RNA polymerase
RT subunit RPB6 are sequence, structural, and functional homologs and
RT promote RNA polymerase assembly.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:892-897(2001).
CC -1- FUNCTION: Promotes RNA polymerase assembly. Latches the N- and C-
CC terminal regions of the beta' subunit thereby facilitating its
CC interaction with the beta and alpha subunits.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA) (N).
CC -1- SUBUNIT: Consists of a sigma factor and the RNAP core enzyme which
CC is composed of 2 alpha chains, 1 beta chain, 1 beta' chain and 1
CC omega chain.
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE OMEGA CHAIN FAMILY.
CC -----
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CC -----
CC EMBL: AJ295839; CAC15848.1; -.
CC PDB: 1HOM; 07-FEB-01.
CC PDB: 1L92; 31-MAY-02.
CC HAMAP: MF_00366; -.
CC DR InterPro: IPR003716; RNA_pol_omega.
CC DR InterPro: IPR006110; RNA_poly_Rpb6.
CC DR Pfam: PF01192; RNA_pol_Rpb6; 1.
CC DR TIGRfam: TIGR00690; rpoZ; 1.
CC KW Transferase; DNA-directed RNA polymerase; Transcription;
CC 3D-structure.
CC FT INIT_MET 0 0
CC FT TURN 3 4
CC FT HELIX 5 11
CC FT HELIX 15 26
CC FT TURN 27 28
CC FT HELIX 29 31
CC FT TURN 32 32
CC FT TURN 35 36
CC FT TURN 40 42
CC FT STRAND 46 46
CC FT TURN 50 51
CC FT STRAND 55 55
CC FT HELIX 59 67
CC FT TURN 68 69
CC FT HELIX 81 86
CC FT TURN 87 90
CC SQ SEQUENCE 98 AA; 11494 MW; 8E4529F14B0C266 CRC64;
Query Match 100.0%; Score 20; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLEP 4
DB 38 VLEP 41

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OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=HB8 / ATCC 27634;
RA Vassilyeva M.N., Lee J., Sekine S., Laptenko O., Kuramitsu S.,
RA Shibata T., Inoue Y., Borukov S., Vassilyev D.G., Yokoyama S.;
RT Purification, crystallization and initial crystallographic analysis
RT of RNA polymerase holoenzyme from Thermus thermophilus.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Promotes RNA polymerase assembly. Latches the N- and C-
CC terminal regions of the beta' subunit thereby facilitating its
CC interaction with the beta and alpha subunits (By similarity).
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA) (N).
CC -1- SUBUNIT: Consists of a sigma factor and the RNAP core enzyme which
CC is composed of 2 alpha chains, 1 beta chain, 1 beta' chain and 1
CC omega chain (By similarity).
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE OMEGA CHAIN FAMILY.
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CC -----
CC EMBL: AB083791; BAB89402.1; -.
CC HAMAP: MF_00366; -.
CC DR InterPro: IPR003716; RNA_pol_omega.
CC DR InterPro: IPR006110; RNA_poly_Rpb6.
CC DR Pfam: PF01192; RNA_pol_Rpb6; 1.
CC DR TIGRfam: TIGR00690; rpoZ; 1.
CC KW Transferase; DNA-directed RNA polymerase; Transcription.
CC SQ SEQUENCE 99 AA; 11505 MW; 824E3933A0912E CRC64;
Query Match 100.0%; Score 20; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLEP 4
DB 39 VLEP 42

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RESULT 8
RPOZ_THETH STANDARD; PRT; 99 AA.
AC O8ROE7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable DNA-directed RNA polymerase omega chain (EC 2.7.7.6)
DE (transcriptase omega chain) (RNA polymerase omega subunit).
DE RPOZ.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;

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RESULT 9
VG6_BPB03 STANDARD; PRT; 100 AA.
AC O37886;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Early protein GP6.
GN 6.
OS Bacteriophage B103.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC Phi-29-like viruses.
OX NCBI_TaxID=10778;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98019084; PubMed=9358052;
RA Recenkova T., Benes V., Paces J., Vlcek C., Paces V.;
RT "Bacteriophage B103: complete DNA sequence of its genome and
RT relationship to other Bacillus phages.";
RL Gene 199:157-163(1997).
CC -1- FUNCTION: ESSENTIAL FOR VIRAL DNA REPLICATION. ACTIVATES THE
CC INITIATION OF DNA REPLICATION BY FORMING A MULTIMERIC
CC NUCLEOPROTEIN COMPLEX AT THE REPLICATION ORIGINS (BY SIMILARITY).
CC -----
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DR EMBL; X99260; CAA67653.1; -
KM Early Protein; DNA replication.
SQ SEQUENCE 100 AA; 11367 MW; DPA32866644580E8 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEP 4
Db 30 VLEP 33

RESULT 10

Y592 CHLPN
ID Y592 CHLPN STANDARD; PRT; 103 AA.
AC 0927M2; 09K2D2; 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical UPF0161 protein CPN0592/CP0156/CPJ0592.
GN CPN0592 OR CP0156 OR CPJ0592.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RA MEDLINE=99206606; PubMed=10192388;
RA Kaiman S., Mitchell W., Marathe R., Lamme C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative Genomes of Chlamydia pneumoniae and C. trachomatis";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RA MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brumham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Baas S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Grimm M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
RT pneumoniae AR39";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RA MEDLINE=20330349; PubMed=10871362;
RA Shira T., Ishii K., Hiraoka H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shira T., Ishii K., Hiraoka H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA";
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
CC -1- SIMILARITY: Belongs to the UPF0161 family.

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DR EMBL; AEO01643; AAD18731.1; -
DR EMBL; AEO02177; AAF38037.1; ALT_INIT.
DR EMBL; AP002547; BAA98799.1; -
DR PIR; E86564; E86564.

DR PIR; H72060; H72060.
DR TIGR; CP0156; -
DR HAMAP; MF_00386; -1.
DR InterPro; IPR002696; DUF37.
DR Pfam; PFI01809; DUF37.1.
DR ProDom; PD004225; DUF37.1.
DR TIGRPFAMs; TIGR00278; TIGR00278; 1.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 103 AA; 11751 MW; CE9CA4852EA15A7C CRC64;

Query Match 100.0%; Score 20; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEP 4
Db 86 VLEP 89

RESULT 11

R13E METVA
ID R13E METVA STANDARD; PRT; 105 AA.
AC P14025;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L30e.
GN RPL30E.
OS Methanococcus vannielii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OX NCBI_TaxID=2187;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1224;
RA MEDLINE=89362493; PubMed=2475640;
RA Lechner K., Heller G., Boeck A.;
RT "Organization and nucleotide sequence of a transcriptional unit of
RT Methanococcus vannielii comprising genes for protein synthesis
RT elongation factors and ribosomal proteins";
RL J. Mol. Evol. 29:20-27(1989).
RN [2]
CC -1- SIMILARITY: BELONGS TO THE L30E FAMILY OF RIBOSOMAL PROTEINS.

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DR EMBL; X15970; CAA34087.1; -
DR PIR; S06621; REMXER.
DR HSSP; P14120; ICN9.
DR HAMAP; MF_00481; -1.
DR InterPro; IPR000231; Ribosomal L30e.
DR InterPro; IPR004038; Ribosomal L7A.
DR Pfam; PFI01248; Ribosomal_L7ae; 1.
DR ProDom; PD004495; Ribosomal_L30e; 1.
DR PROSITE; PS00709; RIBOSOMAL_L30E_1; 1.
DR PROSITE; PS00993; RIBOSOMAL_L30E_2; 1.
KM Ribosomal protein.
SQ SEQUENCE 105 AA; 11515 MW; F1CAF5380E358EC8 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEP 4
Db 91 VLEP 94

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RESULT 12
PRTD HORVU STANDARD; PRT; 106 AA.
ID PRTD HORVU STANDARD; PRT; 106 AA.
AC P12361;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome B6-F complex subunit 4 (17 kDa polypeptide) (Fragment).
GN PRTD.
OS Hordeum vulgare (Barley).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OC NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC STRAIN=CV. Sabarilla;
RX MEDLINE=89240047; PubMed=2654887;
RA Andreeva A.V., Buryakova A.A., Reverdatto S.V., Chakhmakheva O.G.,
RA Efimov V.A.;
RA "Nucleotide sequence of the 5.2 kbp barley chloroplast DNA fragment,
RT containing psbA-psbH-petB-petD gene cluster.";
RL Nucleic Acids Res. 17:2859-2860(1989).
CC -1- FUNCTION: THIS POLYPEPTIDE OF UNKNOWN FUNCTION IS ONE OF THE
CC COMPONENTS OF THE CYTOCHROME B6-F COMPLEX.
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B6-F ARE: CYTOCHROME B6, 17
CC kDa POLYPEPTIDE (PRTD), CYTOCHROME F AND THE RIBSKE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=PI21361-1; Sequence=Displayed;
CC CC
CC Name=Short;
CC IsoId=PI21361-2; Sequence=VSP_001239;
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY. CORRESPONDS TO THE
CC CARBOXYL END OF MITOCHONDRIAL CYTOCHROME B.
CC -----
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CC -----
DR EMBL: X14107; CAA32268.1; -
DR EMBL: X14107; CAA32269.1; -
DR PIR: JN0349; JN0349.
DR InterPro: IPR005870; Cytb6/F_IV.
DR InterPro: IPR005798; Cytb_b6_C.
DR Pfam: PR000032; cytochrome_b_c.1.
DR TIGRfam: TIGR01156; cytb6/F_IV.1.
DR PROSITE: PS00193; CYTOCHROME_B_00; 1.
KW Electron transport; Chloroplast; Photosynthesis; Transmembrane;
KW Alternative splicing.
FT FT 17 MSGSFGWILKSPPII -> MGV (in isoform
FT VARSPIC 1 Short).
FT FT /FTId=VSP_001239.
FT FT
FT NON TER 106 106
FT SEQUENCE 106 AA; 11671 MW; D4D83AE9C47DFD3D CRC64;
SQ
Query Match 100.0%; Score 20; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLEP 4
Db 70 VLEP 73
RESULT 13
YF07_ARCFU STANDARD; PRT; 112 AA.
ID YF07_ARCFU STANDARD; PRT; 112 AA.

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AC 028765;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AF1507.
GN AF1507.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OC NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Kleck H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Richardson D.L., Kierlavage A.R., Graham D.E., Kyriades N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RA "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
CC -----
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CC -----
DR EMBL: AE000998; AAB89743.1; -
DR PIR: B69438; B69438.
DR TIGR: AP1507; -
KW Hypothetical protein; Complete proteome.
KW SEQUENCE 112 AA; 13009 MW; 6C820B43E141B4DB CRC64;
SQ
Query Match 100.0%; Score 20; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLEP 4
Db 82 VLEP 85
RESULT 14
RLA2_EIMTE STANDARD; PRT; 114 AA.
ID RLA2_EIMTE STANDARD; PRT; 114 AA.
AC 096799;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 60S acidic ribosomal protein P2.
OS Eimeria tenella.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriidae; Eimeriidae;
OC Eimeria.
OC NCBI_TaxID=5802;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAPC38;
RA Labbe M., Pery P.;
RT "Molecular cloning of a cDNA encoding an acidic ribosomal protein p2
RT of Eimeria tenella.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION STEP OF
CC PROTEIN SYNTHESIS (By similarity).

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CC -1- SUBUNIT: P1 AND P2 EXIST AS DIMERS AT THE LARGE RIBOSOMAL
CC SUBUNIT (BY SIMILARITY).
CC -1- PTM: PHOSPHORYLATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
CC EMBL: AF353514; AAK38885.1; ALT. INTR.
CC InterPro: IPR001813; 608_ribosomal.
CC Pfam: PF00428; 608_ribosomal; 1.
CC Riboosomal protein; Phosphorylation.
CC KW RIBOSOMAL PROTEIN; PHOSPHORYLATION.
CC SO SEQUENCE 114 AA; 11444 MW; 4C08C3C569078AA9 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEP 4
Db 26 VLEP 29

RESULT 15
MERT ACICA STANDARD; PRT; 116 AA.
ID MERT ACICA STANDARD; PRT; 116 AA.
AC 052106;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mercuric transport protein (Mercury ion transport protein).
GN MERT.
OS Acinetobacter calcoaceticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_Taxid=471;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94134837; Pubmed=8302940;
RA Kholodil G.Y., Lomovskaya O.L., Gorlenko Z.M., Mindlin S.Z.,
RA Yurleva O.V., Nikiforov V.G.;
RT "Molecular characterization of an aberrant mercury resistance
RT transposable element from an environmental Acinetobacter strain.";
RL Plasmid 30:303-308(1993).
-1- FUNCTION: INVOLVED IN MERCURIC TRANSPORT. PASSES A HG(2+) ION
-1- FROM THE PERIPLASMIC MERT PROTEIN TO THE MERCURIC REDUCTASE
(MERA).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (By similarity).
CC -----
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CC -----
CC EMBL: AF213017; AAA19679.1; -
CC InterPro: IPR003457; Transprt_Mert.
CC Pfam: PF02411; Mert; 1.
CC KW Transport; Mercuric resistance; Inner membrane; Mercury; Plasmid;
CC Transmembrane.
CC FT TRANSMEM 16 36 POTENTIAL.
CC FT TRANSMEM 46 66 POTENTIAL.
CC FT TRANSMEM 94 114 POTENTIAL.
CC FT METAL 24 24 HG(2+) (BY SIMILARITY).

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FT METAL 25 25 HG(2+) (BY SIMILARITY).
FT METAL 76 76 HG(2+) (BY SIMILARITY).
FT METAL 82 82 HG(2+) (BY SIMILARITY).
SO SEQUENCE 116 AA; 12510 MW; 2930A92CF8EB810F CRC64;

Query Match 100.0%; Score 20; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEP 4
Db 46 VLEP 49

```

Search completed: November 25, 2003, 13:59:29
Job time : 11 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 13:56:11 / Search time 35 Seconds
(Without alignments)
29.492 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20
Sequence: 1 VLEP 4

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	25	5 Q9BM55	Q9bm55 chione can
2	20	100.0	26	5 Q9BM52	Q9bm52 moniliform
3	20	100.0	30	13 Q9W719	Q9w719 gallus gall
4	20	100.0	43	12 Q9WNU6	Q9wnu6 canine dist
5	20	100.0	47	8 Q95F85	Q95f85 spartina ma
6	20	100.0	47	8 Q95F87	Q95f87 spartina al
7	20	100.0	47	8 Q95F86	Q95f86 spartina an
8	20	100.0	52	2 Q9KRW3	Q9kwr3 pseudomonas
9	20	100.0	54	16 Q8KES4	Q8kes4 chlorobium
10	20	100.0	55	4 Q96FP4	Q96fp4 homo sapien
11	20	100.0	58	12 Q39631	Q39631 calicivir
12	20	100.0	58	12 Q39632	Q39632 calicivir
13	20	100.0	61	12 Q55728	Q55728 chilo iride
14	20	100.0	62	17 Q97US6	Q97us6 sulfolobus
15	20	100.0	63	10 Q9FEX8	Q9fex8 hordeum vul
16	20	100.0	63	16 Q99WL3	Q99wl3 staphylococ

17	20	100.0	63	16 Q8NY88	Q8ny88 staphylococ
18	20	100.0	63	16 Q8COP3	Q8cop3 staphylococ
19	20	100.0	64	2 Q05120	Q05120 methylolact
20	20	100.0	65	3 Q14380	Q14380 schizosacch
21	20	100.0	66	16 Q8G062	Q8g062 bruceella su
22	20	100.0	66	16 Q8F6P0	Q8f6p0 leptospira
23	20	100.0	68	10 Q9ZOK7	Q9zok7 arabidopsis
24	20	100.0	71	13 Q90WY7	Q90wy7 coturnix co
25	20	100.0	71	16 Q8K619	Q8k619 streptococ
26	20	100.0	73	5 Q8T661	Q8t661 trypanosoma
27	20	100.0	74	11 Q9J082	Q9j082 mus musculi
28	20	100.0	76	4 Q8NFR3	Q8nfr3 homo sapien
29	20	100.0	77	2 Q8GMU1	Q8gm1 acinetobact
30	20	100.0	77	16 Q99Q00	Q99q00 streptomyce
31	20	100.0	77	17 Q9YE13	Q9ye13 aeropyrum p
32	20	100.0	79	11 P97585	P97585 rattus norv
33	20	100.0	80	5 Q01970	Q01970 caenorhabdi
34	20	100.0	80	16 Q8P0P9	Q8p0p9 streptococ
35	20	100.0	80	16 Q8FNM6	Q8fnm6 corynebacte
36	20	100.0	81	2 Q8L176	Q8l176 rhodococcus
37	20	100.0	81	12 Q9Q086	Q9q086 canine dist
38	20	100.0	81	17 Q97XS0	Q97xs0 sulfolobus
39	20	100.0	82	8 Q33299	Q33299 zea mays (m
40	20	100.0	82	12 Q89530	Q89530 human heipe
41	20	100.0	83	5 Q18436	Q18436 caenorhabdi
42	20	100.0	83	10 Q8LHJ5	Q8lhj5 oryza sativ
43	20	100.0	83	16 Q8WMD5	Q8wmd5 streptomyce
44	20	100.0	84	12 Q8V4C4	Q8v4c4 hepatitis c
45	20	100.0	84	17 Q8U2X4	Q8u2x4 pyrococcus

ALIGNMENTS

RESULT 1					
Q9BM55	PRELIMINARY;	PRT;	25 AA.		
AC Q9BM55;					
DT 01-JUN-2001 (TEMBLrel. 17, Created)					
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)					
DE LINE-1-like reverse transcriptase (Fragment).					
OS Chione cancellata.					
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;					
OC Veneroidea; Veneridae; Chione.					
OX NCBI_TaxID=145464;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC TRANSPOSON-LRT-L1 retrotransposon;					
RX MEDLINE=20570504; PubMed=11121049;					
RA Arkhipova I., Meselson M.;					
RT "Transposable elements in sexual and ancient asexual taxa.";					
DR Proc. Natl. Acad. Sci. U.S.A. 97:14473-14477(2000).					
DR EMBL; AY013938; AAC59923.1; -					
KW RNA-directed DNA polymerase.					
FT NON_TER	1	1			
FT NON_TER	25	25			
SEQ SEQUENCE	25 AA;	2792 MW;	119E15FE9C4A62A7 CRC64;		
Query Match	100.0%;	Score 20;	DB 5;	Length 25;	
Best Local Similarity	100.0%;	Pred. No. 2.6e+02;			
Matches	4;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
QY	1 VLEP 4				
Db	2 VLEP 5				
RESULT 2					
Q9BM52	PRELIMINARY;	PRT;	26 AA.		
AC Q9BM52;					
DT 01-JUN-2001 (TEMBLrel. 17, Created)					

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE LINE-like reverse transcriptase (Fragment).
 OS Moniliformis moniliformis.
 OC Eukaryota; Metazoa; Acanthocephala; Archicanthocephala;
 OC Moniliformida; Moniliformidae; Moniliformis.
 RN NCBI_TaxID=10237;
 RP SEQUENCE FROM N.A.
 RC TRANSPONSON=LRT-11 retrotransposon;
 RX MEDLINE=20570504; PubMed=11121049;
 RA Arkhipova I., Meselson M.;
 RT "Transposable elements in sexual and asexual taxa";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:14473-14477(2000).
 DR EMBL: AY013942; AAG59926.1; -
 KM RNA-directed DNA polymerase.
 FT NON_TER 1 1
 FT 26 26
 SQ SEQUENCE 26 AA; 2757 MW; 438F0469FPA3CFAD CRC64;

Query Match 100.0%; Score 20; DB 5; Length 26;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEP 4
 ||||
 Db 15 VLEP 18

RESULT 3
 ID 09W719 PRELIMINARY; PRT; 30 AA.
 AC 09W719;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE Polymerase (Fragment).
 GN POL.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
 OC Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 RN NCBI_TaxID=9031;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9922880; PubMed=10364336;
 RA Teang S.K., Switzer W.M., Shanmugam V., Johnson J.A., Goldsmith C.,
 RA Wright A., Fady A., Thea D., Jaffe H., Folks T.M., Henaine W.;
 RT "Evidence of avian leukosis virus subgroup E and endogenous avian
 RT virus in measles and mumps vaccines derived from chicken cells;
 RT investigation of transmission to vaccine recipients";
 RL J. Virol. 73:5843-5851(1999).
 DR EMBL: AF087830; AAD37027.1; -
 FT NON_TER 30 30
 FT 30 30
 SQ SEQUENCE 30 AA; 3401 MW; 6D349EDD72FAC7A CRC64;

Query Match 100.0%; Score 20; DB 13; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEP 4
 ||||
 Db 15 VLEP 18

RESULT 4
 ID 09WNU6 PRELIMINARY; PRT; 43 AA.
 AC 09WNU6;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Fusion protein (Fragment).

GN F.
 OS Canine distemper virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
 RN NCBI_TaxID=11232;
 RP SEQUENCE FROM N.A.
 RA Fickel J., Czupalla O.;
 RT "Canine distemper virus in a badger (Meles meles).";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF152506; AAD38054.2; -
 DR InterPro: IPR000776; Fusion_gly.
 DR Pfam: PF00523; Fusion_gly; 1.
 FT NON_TER 1 1
 FT 43 43
 SQ SEQUENCE 43 AA; 4784 MW; DA940A521273A8C5 CRC64;

Query Match 100.0%; Score 20; DB 12; Length 43;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEP 4
 ||||
 Db 30 VLEP 33

RESULT 5
 ID 09SF85 PRELIMINARY; PRT; 47 AA.
 AC 09SF85;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Ribosomal protein L16 (Fragment).
 GN RPL16.
 OS Spartina maritima.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCD clade; Chloridoideae; Cynodonteae; Spartina.
 RN NCBI_TaxID=49786;
 RP SEQUENCE FROM N.A.
 RA Baumei A., Alnouché M.L., Levasseur J.-E.;
 RT "Molecular investigations in populations of *Spartina anglica* C.E.
 RT Hubbard invading coastal Brittany (France).";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF276970; AAK71926.1; -
 DR InterPro: IPR000114; Ribosomal_L16.
 DR Pfam: PF00252; Ribosomal_L16; 1.
 DR PRINTS: PR00060; RIBOSOMALL16.
 KM Chloroplast.
 FT NON_TER 1 1
 FT 47 47
 FT 47 47
 SQ SEQUENCE 47 AA; 5679 MW; DD8E3D9A67537721 CRC64;

Query Match 100.0%; Score 20; DB 8; Length 47;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEP 4
 ||||
 Db 35 VLEP 38

RESULT 6
 ID 09SF87 PRELIMINARY; PRT; 47 AA.
 AC 09SF87;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Ribosomal protein L16 (Fragment).

GN RPL16.
 OS Spartina alterniflora (smooth cordgrass).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Chloridoideae; Cynodonteae; Spartina.
 ON NCBI_TaxID=29706;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Baumeil A., Ainouche M.L., Levasseur J.-E.;
 RT "Molecular investigations in populations of Spartina anglica C.E.
 RT Hubbard invading coastal Brittany (France).";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF276968; AAK71924.1; -;
 DR InterPro; IPR000114; Ribosomal_L16.
 DR Pfam; PF00252; Ribosomal_L16; I.
 GN Chloroplast.
 KW FT
 FT NON_TER 1 1
 FT NON_TER 47 47
 SQ SEQUENCE 47 AA; 5679 MW; DDBE3D9A67537721 CRC64;

Query Match 100.0%; Score 20; DB 8; Length 47;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4
 ||||
 DB 35 VLEP 38

RESULT 7
 095F86
 ID 095F86 PRELIMINARY; PRT; 47 AA.
 AC 095F86;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
 DE Ribosomal protein L16 (Fragment).
 GN RPL16.
 OS Spartina anglica.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Chloridoideae; Cynodonteae; Spartina.
 ON NCBI_TaxID=49785;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Baumeil A., Ainouche M.L., Levasseur J.-E.;
 RT "Molecular investigations in populations of Spartina anglica C.E.
 RT Hubbard invading coastal Brittany (France).";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF276969; AAK71925.1; -;
 DR InterPro; IPR000114; Ribosomal_L16.
 DR Pfam; PF00252; Ribosomal_L16; I.
 GN Chloroplast.
 KW FT
 FT NON_TER 1 1
 FT NON_TER 47 47
 SQ SEQUENCE 47 AA; 5679 MW; DDBE3D9A67537721 CRC64;

Query Match 100.0%; Score 20; DB 8; Length 47;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4
 ||||
 DB 35 VLEP 38

RESULT 8
 09KMW3
 ID 09KMW3 PRELIMINARY; PRT; 52 AA.
 AC 09KMW3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
 DE Mercuric ion transport protein (Fragment).
 GN MERT.
 OS Pseudomonas putida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 ON NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MT010-2; TRANSPOSON=TN5041D;
 RA Kholodil G.Y., Mindlin S.Z., Gorlenko Z.M., Bass I.A., Kalyaeva E.S.,
 RA Nikiforov V.;
 RT "Host-dependent transposition of TN5041.";
 RL Russ. J. Genet. 36:365-373(2000).
 DR EMBL; Y18977; CAB81562.1; -;
 DR InterPro; IPR003457; Transprt_Mert.
 DR Pfam; PF02411; Mert; I.
 GN FT
 FT NON_TER 52 52
 FT NON_TER 52 52
 SQ SEQUENCE 52 AA; 5209 MW; E6700E9239CB91D CRC64;

Query Match 100.0%; Score 20; DB 2; Length 52;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4
 ||||
 DB 46 VLEP 49

RESULT 9
 08KES4
 ID 08KES4 PRELIMINARY; PRT; 54 AA.
 AC 08KES4;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, last annotation update)
 DE Hypothetical protein CT0608.
 GN CT0608.
 OS Chlorobium tepidum.
 OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
 OC Chlorobium.
 ON NCBI_TaxID=1097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TLS / ATCC 49652 / DSM 12025;
 RX MEDLINE=22103685; PubMed=12093901;
 RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
 RA Dodson R.J., Deboy R., Gwin M.L., Nelson W.C., Haft D.H.,
 RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
 RA Holt I., Mayhew L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
 RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
 RA Vamathevan J., Khouiri H., White O., Gruber T.M., Ketchum K.A.,
 RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
 RT "The complete genome sequence of Chlorobium tepidum TLS, a
 RT photosynthetic, anaerobic, green-sulfur bacterium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
 DR EMBL; AE012834; AAM71850.1; -;
 DR TIGR; CT0608;
 GN Hypothetical protein; Complete proteome.
 SQ SEQUENCE 54 AA; 6056 MW; 79E3572072538A47 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 54;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4
 ||||
 DB 42 VLEP 45

RESULT 10
 096FP4

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ID 096FP4 PRELIMINARY; PRT; 55 AA.
AC 096FP4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE Hypothetical protein.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010607; AAI10607.1; -.
SQ SEQUENCE 55 AA; 6011 MW; 191A7612A78B7EE CRC64;

Query Match 100.0%; Score 20; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
Db 6 VLEP 9

RESULT 11
ID 039631 PRELIMINARY; PRT; 58 AA.
AC 039631;
DT 01-JUN-1998 (TREMBLrel. 05, Created)
DT 01-JUN-1998 (TREMBLrel. 05, Last sequence update)
DE Capsid protein (Fragment).
DE Calicivirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae.
OC NCBI_TaxID=11975;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B453/92/UK;
RX MEDLINE=97278118; PubMed=9131452;
RA Green S.M., Lambden P.R., Owen Caul E., Clarke I.N.;
RT "Capsid sequence diversity in small round structured viruses from
RT recent UK outbreaks of gastroenteritis.";
RL J. Med. Virol. 52:14-19(1997).
DR EMBL; Z73992; CA98298.1; -.
DR InterPro; IPR004005; Calici_coat.
DR Pfam; PF00915; Calici_coat; 1.
FT NON_TER 1
FT NON_TER 58
SQ SEQUENCE 58 AA; 6086 MW; CA987C393B9CC02D CRC64;

Query Match 100.0%; Score 20; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
Db 50 VLEP 53

RESULT 12
ID 039632 PRELIMINARY; PRT; 58 AA.
AC 039632;
DT 01-JUN-1998 (TREMBLrel. 05, Created)
DT 01-JUN-1998 (TREMBLrel. 05, Last sequence update)
DE Capsid protein (Fragment).
DE Calicivirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae.

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OX NCBI_TaxID=11975;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Carmathen/94/UK;
RX MEDLINE=97278118; PubMed=9131452;
RA Green S.M., Lambden P.R., Owen Caul E., Clarke I.N.;
RT "Capsid sequence diversity in small round structured viruses from
RT recent UK outbreaks of gastroenteritis.";
RL J. Med. Virol. 52:14-19(1997).
DR EMBL; Z73997; CA98303.1; -.
DR InterPro; IPR004005; Calici_coat.
DR Pfam; PF00915; Calici_coat; 1.
FT NON_TER 1
FT NON_TER 58
SQ SEQUENCE 58 AA; 6207 MW; A39F892FC412463D CRC64;

Query Match 100.0%; Score 20; DB 12; Length 58;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
Db 50 VLEP 53

RESULT 13
ID 055728 PRELIMINARY; PRT; 61 AA.
AC 055728;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE Hypothetical 7.4 kDa protein.
DE Chilo iridescent virus (CIV) (insect iridescent virus type 6).
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
OC NCBI_TaxID=10488;
RN [1]
RP SEQUENCE FROM N.A.
RA Bahr U., Tidona C.A., Darai G.;
RL Virus Genes 0:0-0(1997).
DR EMBL; AF303741; AAB94439.1; -.
KW Hypothetical protein.
SQ SEQUENCE 61 AA; 7385 MW; 8F718A758C14AE0A CRC64;

Query Match 100.0%; Score 20; DB 12; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
Db 53 VLEP 56

RESULT 14
ID 097US6 PRELIMINARY; PRT; 62 AA.
AC 097US6;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DE Second ORF in transposon ISCI058.
GN SS011456.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OC NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Aways M.J., Chan-Welher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erasuo G., Fletcher C., Gordon P.M.K.,

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RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.,
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.",
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 DR EMBL; AE06883; AAK43026.1; -.
 KW Complete proteome.
 SQ SEQUENCE 62 AA; 6561 MW; 62BCBE0B13F43FF CRC64;

Query Match 100.0%; Score 20; DB 17; Length 62;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEP 4
 ||||
 Db 20 VLEP 23

RESULT 15

Q9FEX8 PRELIMINARY; PRT; 63 AA.
 AC Q9FEX8;
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last annotation update)
 DE Putative lectin (Fragment).
 GN HL#2.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Etiolated coleoptile;
 RA Klopstech K.R.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Etiolated coleoptile;
 RA Grunwald I.;
 RL Thesis (2001), Department of Biological Sciences,
 RL University of Hannover, Hannover, Germany.
 DR EMBL; AJ303112; CAC19669.1; -.
 KW Lectin.
 FT NON_TER 1
 FT NON_TER 63
 SQ SEQUENCE 63 AA; 6948 MW; D794D32B1A5A8C93 CRC64;

Query Match 100.0%; Score 20; DB 10; Length 63;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEP 4
 ||||
 Db 54 VLEP 57

Search completed: November 25, 2003, 14:00:18
 Job time : 36 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 13:46:45 ; Search time 42 Seconds
(without alignments)
15.117 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20
Sequence: 1 VLEP 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_19Jun03:*

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3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
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11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
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20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	4	21	Chemotactic peptid
2	20	100.0	4	22	Adhesion-modulator
3	20	100.0	4	24	Macrophage recruit
4	20	100.0	6	21	Chemotactic peptid
5	20	100.0	7	24	Prostate cancer ma
6	20	100.0	8	17	N-terminus of rece
7	20	100.0	8	17	Fragment of recept
8	20	100.0	8	24	ErbB2 cell overexp
9	20	100.0	9	16	Wheat acetyl-Coenz

10	20	100.0	10	20	AAV07169	HLA binding peptid
11	20	100.0	10	20	AAV07127	HLA binding peptid
12	20	100.0	10	24	ABP71117	Ced-3 protein CARD
13	20	100.0	14	22	AAW00583	Human transcriptio
14	20	100.0	17	21	AAW08085	Amino acid sequenc
15	20	100.0	17	21	AAW08086	Amnio acid sequenc
16	20	100.0	17	24	ABP56417	E. coli val3 relat
17	20	100.0	19	19	AAW70175	Internal peptide f
18	20	100.0	19	22	AAE05631	Internal peptide f
19	20	100.0	20	22	AAW50346	Adeno-associated v
20	20	100.0	25	16	AAW79207	TGF-beta5 residues
21	20	100.0	25	19	AAW67273	Peptide #20 with c
22	20	100.0	26	15	AAW52310	Mouse heavy chain
23	20	100.0	27	22	ABG51099	Human liver peptid
24	20	100.0	27	22	ABG31072	Peptide #3723 enco
25	20	100.0	27	22	ABR36261	Peptide #3767 enco
26	20	100.0	27	22	ABR21633	Peptide #3632 enco
27	20	100.0	27	22	AAW57035	Human brain expres
28	20	100.0	27	22	AAW69425	Human bone marrow
29	20	100.0	27	22	AAW17259	Peptide #3693 enco
30	20	100.0	27	22	AAW29756	Peptide #3793 enco
31	20	100.0	27	22	AAW04951	Peptide #3633 enco
32	20	100.0	27	23	ABG39043	Human peptide enco
33	20	100.0	30	18	AAW24711	Finger 2 domain of
34	20	100.0	34	16	AAW66400	GaINAC-transferase
35	20	100.0	34	18	AAW16483	N-acetylglactosam
36	20	100.0	34	21	AAW02780	Xenopus laevis TGF
37	20	100.0	34	21	AAW92551	Finger 2 subdomain
38	20	100.0	34	22	AAW96570	Human reproductive
39	20	100.0	35	21	AAW89142	Core polypeptide f
40	20	100.0	35	22	ABW05051	Viral DP178/107-11
41	20	100.0	35	22	ABW01977	Viral core polypep
42	20	100.0	35	22	AAW13050	DP178-like/DP107-1
43	20	100.0	35	22	AAW77497	Core polypeptide T
44	20	100.0	36	21	AAW09513	Xenopus TGF-beta 5
45	20	100.0	37	22	ABG58019	Human liver peptid

ALIGNMENTS

RESULT 1
AAB28663
ID AAB28663 strand: peptide; 4 AA.
AC AAB28663;
DT 13-FEB-2001 (first entry)
XX
DE Chemotactic peptide pepu'.
XX
KW Chemotactic; osteopontin; vulnery; antiarthritic; antiporiatic;
KW cytostatic; antitumor; antiinflammatory; osteopathic;
KW wound healing; cell migration; chemotaxis; atherosclerosis; cancer;
KW angiogenic-associated disease; arthritis; psoriasis; haemangioma;
KW ocular neovascularisation; cell apoptosis; nitrous oxide production;
KW inflammation; osteoporosis; immune disease.
XX
OS Mammalia.
OS Synthetic.
XX
PN WO200063247-A2.
PD 26-OCT-2000.
PF 17-APR-2000; 2000WO-US10344.
PR 15-APR-1999; 99US-0129764.
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX Ashkar S;
XX

DR WPI; 2000-687159/67.
XX
PT New osteopontin-derived chemotactic and inhibitory peptides, useful for
PT promoting scarless wound healing; modulating cellular chemotaxis,
PT treating formation of atherosclerotic plaques and preventing metastasis
XX
XX
PS Claim 17; Page 43; 54pp; English.
XX
CC The present sequence is an osteopontin-derived chemotactic peptide.
CC Such chemotactic peptides are useful for promoting scarless wound
CC healing, modulating chemotaxis and promoting cell migration to a target
CC site in a cell of a subject. They are also used for modulating cellular
CC chemotaxis in a mammalian cell such as smooth muscle cell, a macrophage,
CC an endothelial cell, a vascular cell and a tumorigenic cell. They are
CC useful for treating the formation of atherosclerotic plaques in a
CC subject. The peptides are used for preventing metastasis, treating an
CC angiogenic-associated disease such as arthritis, psoriasis, haemangioma,
CC tumour metastasis or ocular neovascularisation. They are also used for
CC activating cell apoptosis, for modulating nitrous oxide production and
CC for inducing chemotaxis. The peptides are useful for diagnosing, treating
CC and preventing tumour metastasis, inflammation, osteoporosis and immune
CC diseases. They can also be used to enhance an immune response by
CC attracting macrophages.
XX
SQ Sequence 4 AA:
Query Match 100.0%; Score 20; DB 21; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLEP 4
Db 1 VLEP 4
RESULT 2
AAB29558
ID AAB29558 standard; peptide; 4 AA.
XX
AC AAB29558;
XX
DT 14-FEB-2001 (first entry)
XX
DE Adhesion-modulatory peptide, SEQ ID NO:15.
XX
KW Adhesion modulatory peptide; target cell adhesion; cell adhesion;
KW endothelial cell; fibroblast; macrophage; neutrophil; myofibroblast;
KW collagen; glycosaminoglycan; extracellular matrix; synthetic substrate;
KW vascular growth; wound healing; keloid formation; scarred; fibrosis;
KW anticoagulant; vulnery; immunomodulatory; antibacterial; anticancer;
KW antitumorigenic; anti-CD4 activity; prosthesis; implant.
XX
OS Synthetic.
XX
PN WO200063236-A2.
XX
PD 26-OCT-2000.
XX
PF 17-APR-2000; 2000WO-US10329.
XX
PR 16-APR-1999; 99US-0129709.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Ashkar S;
XX
DR WPI; 2001-007002/01.
XX
PT Novel adhesive modulatory peptides useful for modulating adhesion of
PT target cells such as endothelial cells, fibroblasts, macrophages to
PT substrate such as polyvinyl surfaces, collagen
XX

PS Claim 8; Page 27; 35pp; English.
XX
CC The invention relates to novel adhesion modulatory peptides (AAB29544-
CC AAB29558) which modulate the adhesion of a target cell to a substrate.
CC The invention also encompasses substrates and devices treated with a
CC peptide of the invention; compositions comprising a peptide of the
CC invention for in vivo use; and analogues, fragments and chemical
CC derivatives of the peptides of the invention. The peptides are useful for
CC modulating the adhesion to a substrate of target cells such as
CC endothelial cells, fibroblasts, macrophages, neutrophils or
CC myofibroblasts. The substrate may be a substrate that is found in the
CC body of a patient, e.g., collagen or hyaluronic acid, or may be a
CC synthetic substrate e.g., a polyvinyl surface, titanium or PGA. The
CC peptides are useful for regulating vessel growth during wound healing
CC and/or in the treatment of damage resulting from vascular disease; for
CC inhibiting or preventing cellular apoptosis; in the treatment of
CC fibrosis; in particular in the clearing of debris; to minimise wound
CC contraction, thereby reducing keloid tissue formation and scarring; and
CC as anti clotting agents. The peptides also have an immunomodulatory
CC effect, and an antibacterial effect by adhering to neutrophils.
CC Additionally, peptides of the invention have an anticancer effect by
CC competing for alpha-v-beta3 integrin binding on the cell surface, and an
CC antitumorigenic effect by having anti-CD4 activity. The peptides are
CC useful for stimulating and/or enhancing cell attachment to polymer
CC scaffolds, to enhance tissue growth and for coating medical devices,
CC including prostheses and implants (e.g., vascular implants). The present
CC sequence represents a specifically claimed adhesion modulatory peptide of
CC the invention.
XX
SQ Sequence 4 AA:
Query Match 100.0%; Score 20; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLEP 4
Db 1 VLEP 4
RESULT 3
ABP58757
ID ABP58757 standard; peptide; 4 AA.
XX
AC ABP58757;
XX
DT 04-APR-2003 (first entry)
XX
DE Macrophage recruitment inhibitor peptide, SEQ ID NO:7.
XX
KW MiniCell display; random peptide library; drug discovery; screening;
KW fusion protein; outer membrane protein;
KW Rickettsia rickettsii 17K antigen; bioactive peptide;
KW macrophage recruitment inhibitor; osteopontin; C5a; fibronectin.
XX
OS Synthetic.
XX
PN WO200272759-A2.
XX
PD 19-SEP-2002.
XX
PF 06-MAR-2002; 2002WO-US06921.
XX
PR 07-MAR-2001; 2001US-274039P.
XX
PR 20-JUL-2001; 2001US-306946P.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Ashkar S;
XX
DR WPI; 2003-046738/04.
XX
PT Minicell display method for screening peptide libraries for peptide
PT

DR WPI; 2000-687159/67.

CC as a highly effective marker for prostate cancer. The novel protein

CC includes a polypeptide that is related to human serum vitamin D
 CC binding protein (VDBP, see ABP58017). The present peptide
 CC corresponds to amino acids 364-370 of this VDBP allele. It is one of
 CC a series of peptides (see ABP58005-16) that distinguish VDBP-related
 CC proteins from other proteins, or which may be characterised as
 CC binding specifically to an anti-VDBP antibody. VDBP-related proteins
 CC are detectable at a higher concentration in serum from a mammal, e.g.
 CC a human, with prostate cancer relative to serum from a healthy
 CC mammal and can therefore be used as prostate cancer markers. They
 CC permit the rapid detection, preferably before metastases occur, of
 CC prostate cancer. A target prostate cancer-associated protein may be
 CC detected using a labelled antibody capable of binding specifically
 CC to the protein. Prostate cancer-associated proteins, and nucleic
 CC acids encoding them, are also useful as targets for treating
 CC prostate cancer, and as indicators for monitoring the efficiency of
 CC prostate cancer therapy.

XX Sequence 7 AA;

Query Match 100.0%; Score 20; DB 24; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
 ||||
 Db 1 VLEP 4

RESULT 6
 AAW06332

ID AAW06332 standard; peptide; 8 AA.

XX AAW06332;

DT 17-JAN-1997 (first entry)

DE N-terminus of receptor-type tyrosine kinase protein ligand.

KM Receptor-type tyrosine kinase; ligand; coomassie staining; PAS staining;

KW N-terminus; human.

OS Homo sapiens.

PN JF0818596-A.

PD 23-JUL-1996.

XX 13-JAN-1995; 95JP-0003677.

XX 09-NOV-1994; 94JP-0275411.

PR 19-OCT-1994; 94JP-0253848.

XX (ASAH) ASAH1 KASEI KOGYO KK.

XX WPI; 1996-388601/39.

PT New ligand for receptor type tyrosine kinase - has mol.wt. 22-25

XX kilo:dalton(s) and is positive for Coomassie and PAS staining

XX Claim 3; Page 43; 51pp; Japanese.

XX This sequence represents the N-terminus of a receptor-type tyrosine
 CC kinase receptor binding ligand of the invention (see AAW06333 and
 CC AAW06334). The ligands of the invention recognise the fragment of the
 CC receptor type kinase receptor represented by AAW06330 (see AAW06331 for
 CC full length sequence). The proteins of the invention have a molecular
 CC weight of 23500 (plus or minus 1500) Da, and are positive for Coomassie
 CC staining and PAS staining. The protein is a new ligand of receptor-type
 CC tyrosine kinases, and can be prepared by standard recombinant
 CC techniques.

XX Sequence 8 AA;

Query Match 100.0%; Score 20; DB 17; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
 ||||
 Db 4 VLEP 7

RESULT 7

AA94654

ID AAR94654 standard; Protein; 8 AA.

XX AAR94654;

DT 18-OCT-1996 (first entry)

DE Fragment of receptor type tyrosine kinase (TK) ligand.

KM Receptor type tyrosine kinase; TK; ligand; differentiation;

KW hematopoietic stem cell; tyrosine; bone marrow; leukaemia.

OS Homo sapiens.

PN WO9611212-A1.

PD 18-APR-1996.

XX 09-OCT-1995; 95WO-JP02069.

XX 22-DEC-1994; 94JP-0320712.

PR 07-OCT-1994; 94JP-024433.

PR 26-OCT-1994; 94JP-0262882.

XX (ASAH) ASAH1 KASEI KOGYO KK.

XX Ohno M, Sakano S;

XX WPI; 1996-209809/21.

PT Ligand peptide binding to receptor-type tyrosine kinase - enhances

PT intracellular tyrosine phosphorylation, useful for investigation of

XX undifferentiated blood cell behaviour

XX Disclosure; Page 162; 193pp; Japanese.

XX A ligand polypeptide which binds to the extracellular part of a
 CC specific receptor-type tyrosine kinase and induces phosphorylation
 CC of tyrosine within the cell can be used in the study of the
 CC differentiation of blood cells such as the haematopoietic stem
 CC cells; of disease processes such as leukaemia, and of the biology of
 CC bone marrow transplantation. The ligand plays a role in the
 CC differentiation process and the specific ligand target is expressed
 CC in undifferentiated blood cells.

XX Sequence 8 AA;

Query Match 100.0%; Score 20; DB 17; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
 ||||
 Db 4 VLEP 7

RESULT 8

ABP9157

ID ABP9157 standard; Peptide; 8 AA.

XX ABP9157;

DT 18-MAR-2003 (first entry)

XX ErBb2 cell overexpression EOP1-130 peptide SEQ ID NO:203.
DE
XX
XX ErBb2: cancer; oncogene; ErBb2 overexpression-associated protein isoform;
KM EOP1; EOP; ErBb2 overexpression feature; cytostatic; vaccine;
KM gene therapy.
XX
XX Homo sapiens.
OS
XX
XX MO200290991-A2.
PN
XX
XX 14-NOV-2002.
PD
XX
XX 02-MAY-2002; 2002WO-GB02047.
PF
XX
XX 03-MAY-2001; 2001GB-0010886.
PR
XX 23-NOV-2001; 2001GB-0028183.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA
XX
XX Herath HMAc, Page Mj;
PI
XX
XX WPI; 2003-103531/09.
DR
XX
XX Diagnosing and treating ErBb2-related cancer, comprises generating
PT ErBb2 Overexpression Features (EOPs) from test samples from a subject
PT by electrophoresis, and comparing the EOPs in the sample with a
PT predetermined reference range -
XX
XX
XX Claim 3; Page 23; 106pp; English.
PS
XX
XX The present invention describes a method for screening or diagnosing
CC ErBb2-related cancer. The method comprises generating ErBb2
CC overexpression features (EOPs) from test samples of body fluid from the
CC subject by electrophoresis, and comparing the EOPs in the test sample
CC with that from normal subjects or with an expression reference feature
CC (ERF) in the test sample. Also described: (1) an antibody capable of
CC immunospecific binding to an ErBb2 overexpression protein isoform
CC (EOP1); (2) pharmaceutical compositions comprising an EOP1, a nucleic
CC acid encoding an EOP1, an amount of the above antibody or its fragment,
CC and a carrier; (3) a kit comprising one or more antibodies and/or EOPs
CC cited above; other reagents and instructions for use; (4) methods of
CC treating or preventing ErBb2-related cancer; (5) methods of screening
CC for or identifying agents that interact with or modulate the expression
CC or activity of one or more EOPs; EOP1 fragment, EOP1-related
CC polypeptides, or EOP1-fusion proteins; (6) a method for modulating the
CC activity of one or more of the ErBb2 EOPs, comprising administering to
CC a subject an agent identified by the method of (5); and (7) a method for
CC identifying targets for therapeutic modulation of ErBb2-related cancer.
CC EOPs have cytostatic activity and can be used in vaccines and gene
CC therapy. The method is useful in screening, diagnosing, preventing or
CC treating ErBb2-related cancer, determining the stage or severity of
CC ErBb2-related cancer, identifying a subject at risk of developing
CC ErBb2-related cancer, monitoring the effect of therapy administered to
CC a subject with ErBb2-related cancer, and for drug screening or drug
CC development. The kit is useful in carrying out the above methods.
CC ABP9940 to ABP99206 represent specifically claimed EOPs from the
CC present invention.
XX
XX
SQ Sequence 8 AA;
XX
XX
XX Query Match 100.0%; Score 20; DB 24; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
|||
Db 2 VLEP 5
|||
RESULT 9
AAR84629
ID AAR84629 standard; Peptide; 9 AA.

XX
AC AAR84629;
XX
XX
DT 02-JUN-1996 (first entry)
XX
XX
DE Wheat acetyl-Coenzyme-A-carboxylase peptide sequence.
XX
XX Acetyl Coenzyme A carboxylase; ACCase; plasmid pK111;
KM transgenic plant; modified oil content;
KM polyhydroxyalkanoate polymer; herbicide resistance;
KW monocot crop improvement.
XX
XX
XX Triticum aestivum.
OS
XX
XX MO9529246-A1.
PN
XX
XX 02-NOV-1995.
PD
XX
XX 21-APR-1994; 94WO-GB00846.
PF
XX
XX 21-APR-1994; 94WO-GB00846.
PR
XX
XX (ZENNE) ZENNECA LTD.
PA
XX
XX Bright SWJ, Elborough KM, Fentem PA, Slabas AR;
PI
XX
XX WPI; 1995-382994/49.
DR
XX
XX DNA encoding acetyl Coenzyme A carboxylase - used for developing
PT plants with controlled expression of ACCase, e.g. for controlling
PT fatty acid synthesis.
XX
XX
PS Disclosure; Fig 3; 61pp; English.

XX
XX Wheat acetyl Coenzyme A carboxylase (ACCase) was partially
CC purified from wheat germ and a dominant 220 KDa band was identified
CC as ACCase by column chromatography and SDS-PAGE. After
CC purification in the gel, the protein was hydrolysed using
CC Endoproteinase LysC, and resulting peptides were purified by
CC electrophoresis and loaded onto an ABI 477A pulse liquid
CC protein sequencer. Sequence data of 4 peptides (this peptide and
CC peptides AAR84625, AAR84627 and AAR84631) were compared with plasmid
CC pK111-deduced amino acid sequences (AAR84630, AAR84626, AAR84628 and
CC AAR84632) so as to authenticate pK111 (see AAT04948) as wheat ACCase
CC partial cDNA. More specifically, this peptide corresponds to
CC amino acids 319-327 of the pK111 deduced AA sequence AAR84619
CC (i.e. AAR84630). Partial cDNA clone pK11 (NCIB 40553) can be
CC used to create a sense/antisense expression cassette to
CC transform rape and other oilseed plants (canola, soybean,
CC sunflower) to downregulate production of the ACCase enzyme.
CC The transgenic plants have a lower or a modified oil content.
CC Down-regulation of oil synthesis can be used to divert the
CC substrate, acetyl Coenzyme A, into synthesis of alternative
CC storage materials (starch, protein or novel polymers e.g.
CC polyhydroxyalkanoates). Full-length ACCase clones can be used
CC to create transgenic plants over-expressing ACCase, and
CC therefore with increased oil content. ACCase over-expression in
CC monocot plants such as wheat, barley, maize and rice, which are
CC normally sensitive to herbicides, results in
CC arylloxyphenoxy-propionate and alkylketone herbicide resistance in
CC the transgenic plants (dicots are normally resistant to these
CC herbicides).

QY 1 VLEP 4
|||
Db 2 VLEP 5
|||
Query Match 100.0%; Score 20; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
|||
Db 2 VLEP 5
|||

```

RESULT 10
AAV07169
ID AAV07169 standard; Peptide; 10 AA.
XX
XX AC AAV07169;
XX
XX 02-JUL-1999 (first entry)
XX
XX HLA binding peptide.
XX
XX Cancer associated antigen; diagnosis; research; treatment; human;
XX breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
XX prostate cancer.
XX
XX Homo sapiens.
XX
XX WO9904265-A2.
XX
XX 28-JAN-1999.
XX
XX 15-JUL-1998; 98WO-US14679.
XX
XX 22-JUN-1998; 98US-0102322.
XX 17-JUL-1997; 97US-0896164.
XX 10-OCT-1997; 97US-0061599.
XX 10-OCT-1997; 97US-0061765.
XX 10-OCT-1997; 97US-0948705.
XX 11-OCT-1997; 97GB-0021697.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Chen Y, Gout I, Gure A, O'Hare M, Obata Y, Old LJ;
XX Pfreundschuh M, Sahin U, Scanlan MJ, Stockert E;
XX Tureci O;
XX WPI; 1999-132448/11.
XX
XX New isolated cancer associated nucleic acids and polypeptides -
XX isolated using sera from cancer patients, used to develop products
XX for the diagnosis, monitoring or treatment of cancers
XX
XX Example 16; Page 762; 787pp; English.
XX
XX The invention relates to a method for diagnosing a disorder characterised
XX by expression of a human cancer associated antigen precursor coded for by
XX a nucleic acid molecule (NAM). The method comprises: (a) contacting a
XX biological sample isolated from a subject with an agent that specifically
XX binds to the NAM, an expression product or a fragment of an expression
XX product complexed with an HLA molecule; and (b) determining the
XX interaction between the agent and the NAM or the expression product as a
XX determination of the disorder. The products and methods can be used in
XX the diagnosis, monitoring, research, or treatment of conditions
XX characterised by the expression of various cancer associated antigens.
XX The invention provides nucleic acid sequences and encoded polypeptides
XX which are cancer associated antigen precursors expressed in human breast
XX cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
XX lung cancer.
XX
XX Sequence 10 AA;
XX
XX Query Match 100.0%; Score 20; DB 20; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VLEP 4
XX ||||
XX Db 5 VLEP 8
XX
XX RESULT 11
XX AAV07127
XX ID AAV07127 standard; Peptide; 10 AA.

```

```

XX
XX AC AAV07127;
XX
XX 02-JUL-1999 (first entry)
XX
XX HLA binding peptide.
XX
XX Cancer associated antigen; diagnosis; research; treatment; human;
XX breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
XX prostate cancer.
XX
XX Homo sapiens.
XX
XX WO9904265-A2.
XX
XX 28-JAN-1999.
XX
XX 15-JUL-1998; 98WO-US14679.
XX
XX 22-JUN-1998; 98US-0102322.
XX 17-JUL-1997; 97US-0896164.
XX 10-OCT-1997; 97US-0061599.
XX 10-OCT-1997; 97US-0061765.
XX 10-OCT-1997; 97US-0948705.
XX 11-OCT-1997; 97GB-0021697.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Chen Y, Gout I, Gure A, O'Hare M, Obata Y, Old LJ;
XX Pfreundschuh M, Sahin U, Scanlan MJ, Stockert E;
XX Tureci O;
XX WPI; 1999-132448/11.
XX
XX New isolated cancer associated nucleic acids and polypeptides -
XX isolated using sera from cancer patients, used to develop products
XX for the diagnosis, monitoring or treatment of cancers
XX
XX Example 16; Page 755; 787pp; English.
XX
XX The invention relates to a method for diagnosing a disorder characterised
XX by expression of a human cancer associated antigen precursor coded for by
XX a nucleic acid molecule (NAM). The method comprises: (a) contacting a
XX biological sample isolated from a subject with an agent that specifically
XX binds to the NAM, an expression product or a fragment of an expression
XX product complexed with an HLA molecule; and (b) determining the
XX interaction between the agent and the NAM or the expression product as a
XX determination of the disorder. The products and methods can be used in
XX the diagnosis, monitoring, research, or treatment of conditions
XX characterised by the expression of various cancer associated antigens.
XX The invention provides nucleic acid sequences and encoded polypeptides
XX which are cancer associated antigen precursors expressed in human breast
XX cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
XX lung cancer.
XX
XX Sequence 10 AA;
XX
XX Query Match 100.0%; Score 20; DB 20; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VLEP 4
XX ||||
XX Db 5 VLEP 8
XX
XX RESULT 12
XX ABP71117
XX ID ABP71117 standard; peptide; 10 AA.
XX
XX AC ABP71117;
XX
XX 14-APR-2003 (first entry)

```



```

XX DE Ced-3 protein CARD region fragment.
XX XX
XX BTF3; cell death; apoptosis; basic transcription factor; cytosolic;
XX KM neurotropic; neuroprotective; antiparkinsonian; antiarteriosclerotic;
XX KM antirheumatic; antiarthritic; gene therapy; CARD; ced-3.
XX OS
XX Unidentified.
XX FH
XX Key Location/Qualifiers
XX FT Misc-difference 10 /note="unknown"
XX PN WO200295001-A2.
XX XX
XX 28-NOV-2002.
XX PD
XX 21-MAY-2002; 2002WO-US16230.
XX PF
XX 21-MAY-2001; 2001US-292559P.
XX PR
XX (REGC ) UNIV CALIFORNIA.
XX PA
XX Rothman JH, Bloss T, Wiltze E;
XX PI
XX WPI; 2003-167228/16.
XX DR
XX
XX PT Inhibiting or increasing programmed cell death of a cell, for treating
XX PT e.g. cancer, comprises upregulating or inhibiting, respectively, the
XX PT expression or activity of basic transcription factor (BTF3 or its
XX PT homolog in the cell -
XX PS
XX Examples; Fig 2A; 84pp; English.
XX
XX CC The invention relates to inhibiting or increasing programmed cell death
XX CC of a cell. The method involves upregulating or inhibiting, respectively,
XX CC the expression or activity of basic transcription factor (BTF3 or its
XX CC homologue in the cell. The BTF3 polypeptides and nucleic acids are useful
XX CC for inhibiting or increasing programmed cell death. They are used for
XX CC screening for an agent that increases or inhibits programmed cell death
XX CC or pre-screening for an agent that modulates programmed cell death. The
XX CC screened agent that increases or inhibits programmed cell death, is used
XX CC for diagnosing or treating cancer or neurodegenerative diseases (e.g.
XX CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease
XX CC or multiple sclerosis), atherosclerosis, or rheumatoid arthritis.
XX CC Sequences ABP71106-123 represent CARD regions of various CARD proteins.
XX
XX SQ Sequence 10 AA;

```

```

Query Match          100.0%; Score 20; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      1 VLEP 4
        ||||
        6 VLEP 9
Db

```

```

RESULT 13
AAM00583
ID AAM00583 standard; Peptide; 14 AA.
XX
XX AAM00583;
XX
XX 01-OCT-2001 (first entry)
XX DE Human transcription factor fragment SEQ ID NO: 1131.
XX DE
XX Human; single nucleotide polymorphism; SNP; paternity test;
XX KM forensic test; aberrant protein expression.
XX OS
XX Homo sapiens.
XX

```

```

PN WO200151670-A2.
XX
XX 19-JUL-2001.
XX PD
XX 05-JAN-2001; 2001WO-US00322.
XX PF
XX 07-JAN-2000; 2000US-0174962.
XX PR
XX (CURA-) CURAGEN CORP.
XX PA
XX Shimkets RA, Leach MD;
XX PI
XX WPI; 2001-451871/48.
XX DR
XX N-PSDB; AAH89700.
XX
XX PT Isolated human polynucleotides containing single nucleotide
XX PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
XX PT infection and diabetes -
XX PS
XX Disclosure; Page 427; 475pp; English.
XX
XX CC The present invention relates to human nucleic acids containing single
XX CC nucleotide polymorphisms (SNPs). These can be used in forensic and
XX CC paternity tests, and to aid in the treatment of diseases associated with
XX CC aberrant protein expression, including cancer, amyloidosis, diabetes,
XX CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
XX CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
XX CC meningitis, muscular disorders, dementia, neurological diseases, tubercous
XX CC osteoporosis, male infertility, hypercalcaemia, blood pressure disorders,
XX CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
XX CC autoimmunity. The present sequence is a peptide encoded by a
XX CC polymorphism-containing oligonucleotide fragment of the invention.
XX
XX SQ Sequence 14 AA;

```

```

Query Match          100.0%; Score 20; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 VLEP 4
        ||||
        5 VLEP 8
Db

```

```

RESULT 14
AAB08085
ID AAB08085 standard; peptide; 17 AA.
XX
XX AAB08085;
XX
XX 04-DEC-2000 (first entry)
XX DE Amino acid sequence of a helper T cell epitope from CDV.
XX DE
XX T helper cell epitope; CDV; immune response; canine vaccine.
XX KM
XX Canine distemper virus.
XX OS
XX WO200046390-A1.
XX PN
XX 10-AUG-2000.
XX PD
XX 07-FEB-2000; 2000WO-AU00070.
XX PF
XX 05-FEB-1999; 99AU-0008533.
XX PR
XX 04-AUG-1999; 99AU-0002013.
XX
XX (UYME ) UNIV MELBOURNE.
XX PA (CSLC-) CSL LTD.
XX PA (CSTR ) COMMONWEALTH SCI & IND RES ORG.
XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
XX PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX

```

PI Jackson DC, Souravi G, Walker J;
 XX WPI; 2000-532904/48.
 XX Novel T helper cell epitopes derived from canine distemper virus useful
 PT for preparation of canine vaccines
 XX
 PS Claim 1; Page 28; 54pp; English.
 XX
 CC AAB08076-B08101 represent T helper cell epitopes, derived from canine
 CC distemper virus (CDV). Compositions comprising these T cell helper
 CC epitopes are useful for inducing an immune response in an animal. The
 CC epitopes are useful as components of animal, in particular, canine
 CC vaccines, either simply as synthetic peptide based vaccines and as
 CC additions to vaccines containing more complex antigens.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 20; DB 21; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLEP 4
 Db 13 VLEP 16
 RESULT 15
 AAB08086
 ID AAB08086 standard; peptide; 17 AA.
 XX
 AC AAB08086;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Amino acid sequence of a helper T cell epitope from CDV.
 XX
 KM T helper cell epitope; CDV; immune response; canine vaccine.
 OS Canine distemper virus.
 XX
 PN WO200046390-A1.
 XX
 PD 10-AUG-2000.
 XX
 PF 07-FEB-2000; 2000WO-AU00070.
 XX
 PR 05-FEB-1999; 99AU-0008533.
 PR 04-AUG-1999; 99AU-0002013.
 XX
 PA (UYME) UNIV MELBOURNE.
 PA (CSLC-) CSL LTD.
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 PA (HALL-) HALT INST MEDICAL RES WALTER & ELIZA.
 XX
 PI Jackson BC, Souravi G, Walker J;
 XX
 DR WPI; 2000-532904/48.
 XX
 PT Novel T helper cell epitopes derived from canine distemper virus useful
 PT for preparation of canine vaccines -
 XX
 PS Claim 1; Page 28; 54pp; English.
 XX
 CC AAB08076-B08101 represent T helper cell epitopes, derived from canine
 CC distemper virus (CDV). Compositions comprising these T cell helper
 CC epitopes are useful for inducing an immune response in an animal. The
 CC epitopes are useful as components of animal, in particular, canine
 CC vaccines, either simply as synthetic peptide based vaccines and as
 CC additions to vaccines containing more complex antigens.
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 20; DB 21; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLEP 4
 Db 6 VLEP 9
 Search completed: November 25, 2003, 13:59:06
 Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 13:58:16 / Search time 22 Seconds
(without alignments)
7.693 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20

Sequence: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6CTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/6backfill1.pep:*

Pred. No. is the number of results predicted by the chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	9	4	US-08-737-109-5
2	20	100.0	19	3	US-08-928-213B-35
3	20	100.0	19	3	US-09-001-984C-72
4	20	100.0	19	4	US-09-396-347F-72
5	20	100.0	25	1	US-08-127-909-20
6	20	100.0	25	2	US-08-457-353-20
7	20	100.0	25	3	US-09-011-525-5
8	20	100.0	26	1	US-07-942-245-281
9	20	100.0	26	4	US-08-525-539A-21
10	20	100.0	34	2	US-08-967-508-1
11	20	100.0	34	3	US-08-967-508-1
12	20	100.0	34	5	PCT-US94-02552-1
13	20	100.0	35	3	US-09-082-279B-504
14	20	100.0	35	4	US-09-315-304B-504
15	20	100.0	35	4	US-09-834-784-504
16	20	100.0	40	4	US-09-314-268-106
17	20	100.0	65	6	5320958-17
18	20	100.0	70	4	US-09-134-001C-4579
19	20	100.0	74	4	US-09-107-532A-4364
20	20	100.0	75	3	US-08-928-383B-13
21	20	100.0	82	4	US-09-655-270A-25
22	20	100.0	84	4	US-09-464-535-18
23	20	100.0	90	4	US-09-252-991A-29776
24	20	100.0	93	3	US-09-208-804-3
25	20	100.0	93	3	US-08-801-743-3
26	20	100.0	98	3	US-08-478-097A-5
27	20	100.0	98	4	US-09-496-398-5

28	20	100.0	100	2	US-08-963-601-2	Sequence 2, Appl
29	20	100.0	100	4	US-08-735-848-2	Sequence 2, Appl
30	20	100.0	101	4	US-09-216-393B-114	Sequence 114, Ap
31	20	100.0	101	4	US-09-216-393B-268	Sequence 268, Ap
32	20	100.0	105	3	US-08-488-551B-639	Sequence 639, Ap
33	20	100.0	105	4	US-09-732-210-1021	Sequence 1021, Ap
34	20	100.0	106	4	US-09-198-452A-6845	Sequence 6845, Ap
35	20	100.0	108	3	US-08-388-353-639	Sequence 639, Ap
36	20	100.0	109	4	US-09-328-352-4485	Sequence 4485, Ap
37	20	100.0	111	4	US-09-198-452A-1159	Sequence 1159, Ap
38	20	100.0	112	3	US-08-927-433-7	Sequence 7, Appl
39	20	100.0	114	1	US-08-481-377-27	Sequence 27, Appl
40	20	100.0	114	2	US-08-491-835-25	Sequence 25, Appl
41	20	100.0	114	3	US-09-153-733A-27	Sequence 27, Appl
42	20	100.0	114	3	US-08-946-092A-25	Sequence 25, Appl
43	20	100.0	114	3	US-09-172-062-25	Sequence 25, Appl
44	20	100.0	114	4	US-09-301-520D-25	Sequence 25, Appl
45	20	100.0	114	4	US-09-389-705-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-08-737-109-5
Sequence 5, Application US/08737109
Patent No. 6455688
GENERAL INFORMATION:
APPLICANT: SLABAS, Antoni Ryszard
APPLICANT: ELBOROUGH, Kieran Michael
APPLICANT: BRIGHT, Simon William Jonathan
APPLICANT: FENTON, Philip Anthony
TITLE OF INVENTION: Plant Gene Specifying Acetyl Coenzyme A
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,109
FILING DATE: 21-OCT-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/00846
FILING DATE: 02-MAY-1994
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Peptide
HYPOTHEICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Avena sativa
US-08-737-109-5

Query Match 100.0%, Score 20, DB 4, Length 9;
Best local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
VLEP 4
VLEP 5

RESULT 2
US-08-928-213B-35
; Sequence 35, Application US/08928213B
; Patent No. 6238905
; GENERAL INFORMATION:
; APPLICANT: McHenry, Charles S.
; Seville, Mark
; Cull, Millard G.
; TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III
; HOLOENZYME
; NUMBER OF SEQUENCES: 195
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,213B
; FILING DATE: 12-Sep-1997
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: ENZYCO-02550
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-705-8410
; TELEFAX: 415-397-8338
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-08-928-213B-35

Query Match 100.0%; Score 20; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
|||
Db 1 VLEP 4

RESULT 3
US-09-001-984C-72
; Sequence 72, Application US/09001984C
; Patent No. 6245331
; GENERAL INFORMATION:
; APPLICANT: Laal, Suman
; APPLICANT: Zolla-Pazner, Susan
; APPLICANT: Belisle, John T.
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
; FILE REFERENCE: NYU-011
; CURRENT APPLICATION NUMBER: US/09/001,984C
; CURRENT FILING DATE: 1997-12-31
; PRIOR APPLICATION NUMBER: 60/034,003
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 72
; LENGTH: 19
; TYPE: PRT

; ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-001-984C-72

Query Match 100.0%; Score 20; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
|||
Db 15 VLEP 18

RESULT 4
US-09-396-347F-72
; Sequence 72, Application US/09396347F
; Patent No. 6506384
; GENERAL INFORMATION:
; APPLICANT: Laal, Suman
; APPLICANT: Zolla-Pazner, Susan
; APPLICANT: Belisle, John T.
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
; FILE REFERENCE: 32004-169276
; CURRENT APPLICATION NUMBER: US/09/396,347F
; CURRENT FILING DATE: 1999-09-14
; PRIOR APPLICATION NUMBER: 09/001,984
; PRIOR FILING DATE: 1997-12-31
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 72
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-396-347F-72

Query Match 100.0%; Score 20; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
|||
Db 15 VLEP 18

RESULT 5
US-08-127-909-20
; Sequence 20, Application US/08127909
; Patent No. 5436228
; GENERAL INFORMATION:
; APPLICANT: Postlethwaite, Arnold E.
; APPLICANT: Seyer, Jerome
; APPLICANT: Kang, Andrew
; TITLE OF INVENTION: CHEMOTACTIC WOUND HEALING PEPTIDES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,909
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 90202

TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-127-909-20

Query Match 100.0%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
|||
Db 4 VLEP 7

RESULT 6
US-08-457-353-20
Sequence 20, Application US/08457353
Patent No. 5824647
GENERAL INFORMATION:
APPLICANT: Postlethwaite, Arnold E.
APPLICANT: Seyer, Jerome
TITLE OF INVENTION: CHEMOTACTIC WOUND HEALING PEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,353
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 90202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-457-353-20

Query Match 100.0%; Score 20; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
|||
Db 4 VLEP 7

RESULT 7

US-09-011-525-5
Sequence 5, Application US/09011525
Patent No. 6020172
GENERAL INFORMATION:
APPLICANT: BOTH, GERALD W.
TITLE OF INVENTION: GENE THERAPY USING OVINE ADENOVIRAL VECTORS
FILE REFERENCE: Gene Therapy Using Ovine Adenoviral Ve
CURRENT APPLICATION NUMBER: US/09/011,525
CURRENT FILING DATE: 1998-04-20
EARLIER APPLICATION NUMBER: PCT/AU96/00518
EARLIER FILING DATE: 1996-08-14
EARLIER APPLICATION NUMBER: AU PN4776
EARLIER FILING DATE: 1995-08-14
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 5
LENGTH: 25
TYPE: PRT
ORGANISM: Ovine adenovirus
US-09-011-525-5

Query Match 100.0%; Score 20; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
|||
Db 7 VLEP 10

RESULT 8
US-07-942-245-281
Sequence 281, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 281:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-281

Query Match 100.0%; Score 20; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEP 4
|||
Db 5 VLEP 8

RESULT 9

US-08-525-539A-21
Sequence 21, Application US/08525539A
Patent No. 6309636
GENERAL INFORMATION:
APPLICANT: DO COUTO, FERNANDO J.R.
APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-525-539A-21

Query Match 100.0%; Score 20; DB 4; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEP 4
|||
Db 1 VLEP 4

RESULT 10

US-08-967-508-1
Sequence 1, Application US/08967508
Patent No. 5910570
GENERAL INFORMATION:
APPLICANT: The Upjohn Company
APPLICANT: FOR U.S. PURPOSES ONLY: Elhammer, Ake P. and Homa, Fred L.
TITLE OF INVENTION: A Cloned DNA Encoding a UDP-GALNAc:
TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn Company, Intellectual
ADDRESSEE: Property Legal Services

STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,508
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,830
FILING DATE: 13 No. 5910570ember 1995
ATTORNEY/AGENT INFORMATION:
NAME: Darnley Jr., James D.
REGISTRATION NUMBER: 33,673
REFERENCE/DOCKET NUMBER: 4755.P CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-833-2210
TELEFAX: 616-833-8897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-967-508-1

Query Match 100.0%; Score 20; DB 2; Length 34;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEP 4
|||
Db 7 VLEP 10

RESULT 11

US-08-967-506-1
Sequence 1, Application US/08967506
Patent No. 6096512
GENERAL INFORMATION:
APPLICANT: The Upjohn Company
APPLICANT: FOR U.S. PURPOSES ONLY: Elhammer, Ake P. and Homa, Fred L.
TITLE OF INVENTION: A Cloned DNA Encoding a UDP-GALNAc:
TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn Company, Intellectual
ADDRESSEE: Property Legal Services
STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,506
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,830
FILING DATE: 13 No. 6096512ember 1995

ATTORNEY/AGENT INFORMATION:
NAME: Darnley Jr., James D.
REGISTRATION NUMBER: 33,673
REFERENCE/DOCKET NUMBER: 4755.P CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-833-2210
TELEFAX: 616-833-8897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-967-506-1

Query Match 100.0%; Score 20; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
Db 7 VLEP 10

RESULT 12
PCT-US94-02552-1
Sequence 1, Application PC/TUS9402552
GENERAL INFORMATION:
APPLICANT: Elhammer, Ake P.
TITLE OF INVENTION: A Cloned DNA Encoding a UDP-GalNAc:
NUMBER OF INVENTIONS: Polypeptide, N-Acetylglucosaminyltransferase
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Upjohn Company, Corp. Intellectual
ADDRESS: Property Law
STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02552
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Darnley Jr., James D.
REGISTRATION NUMBER: 33,673
REFERENCE/DOCKET NUMBER: 4755.P CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-385-5210
TELEFAX: 616-385-6897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US94-02552-1

Query Match 100.0%; Score 20; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
Db 7 VLEP 10

RESULT 13
US-09-082-279B-504
Sequence 504, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohmed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 504
LENGTH: 35
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-504

Query Match 100.0%; Score 20; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
Db 13 VLEP 16

RESULT 14
US-09-315-304B-504
Sequence 504, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 504
LENGTH: 35
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-315-304B-504

Query Match 100.0%; Score 20; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
Db 13 VLEP 16

RESULT 15
US-09-834-784-504
; Sequence 504, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/834,784
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ. ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-834-784-504

Query Match 100.0%; Score 20; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 VLEP 4
|||
Db 13 VLEP 16

Search completed: November 25, 2003, 14:01:26
Job time : 23 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 14:05:07 ; Search time 21 Seconds
(without alignments)
18.318 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20
Sequence: 1 VLEP 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 86

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 76:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	60.0	3	A33802	thyrotropin-releas
2	11	55.0	4	I51049	metallothionein-A
3	10	50.0	4	E44823	synaptosomal-assoc
4	8	40.0	4	A02147	phagocytosis-stimu
5	7	35.0	3	RHTDJO	thyroliberin - Bom
6	7	35.0	3	RHSGT	thyroliberin - pig
7	7	35.0	3	RHSMT	thyroliberin - she
8	7	35.0	3	A92971	thyroliberin - eae
9	7	35.0	3	A43391	TRH-like tripeptid
10	7	35.0	3	I78890	tyrosine protein k
11	7	35.0	4	A32039	tyrosine-melanocyt
12	7	35.0	4	PL0140	carbon-monoxide de
13	7	35.0	4	A61300	22k superhelical D
14	7	35.0	4	I57745	D-mannosate hydrol
15	7	35.0	4	S53508	starvation-induced
16	7	35.0	4	S17255	ribosomal protein
17	7	35.0	4	A34626	RPCH-related neuro
18	7	35.0	4	PT0240	ig heavy chain CRD
19	7	35.0	4	I54357	schwannomin - mous
20	7	35.0	4	PT0675	T-cell receptor be
21	6	30.0	4	A48360	gamma subunit of p
22	6	30.0	4	A27897	glucan 1,4-alpha-g
23	5	25.0	4	A41890	protein D - Escher
24	5	25.0	4	B43848	cell surface adhes
25	5	25.0	4	I40505	hypothetical prote
26	5	25.0	4	PT0677	T-cell receptor be
27	5	25.0	4	A26209	protein-glutamine
28	5	25.0	4	S55238	pallidipin - assas
29	4	20.0	3	PQ0010	angiotensin-conver

30	4	20.0	3	T13892	cytochrome-c oxida
31	4	20.0	4	S18401	thyroglobulin - do
32	4	20.0	4	A37832	phenol 2-monooxyge
33	4	20.0	4	T46627	hypothetical prote
34	4	20.0	4	T30569	hypothetical prote
35	4	20.0	4	T38888	COI intron 16 prot
36	4	20.0	4	A35779	neuropeptide Antho
37	4	20.0	4	A53284	T-cell receptor be
38	4	20.0	4	PT0645	T-cell receptor be
39	4	20.0	4	PT0721	T-cell receptor be
40	4	20.0	4	A40135	branched-chain-aml
41	4	20.0	4	S47552	ubiquitin - rat
42	4	20.0	4	S09478	globulin IV alpha
43	3	15.0	3	B23751	spinal cord peptid
44	3	15.0	3	S13894	histidinol dehydro
45	3	15.0	4	I40870	phospholipase C (E

ALIGNMENTS

RESULT 1

A33802
thyrotropin-releasing hormone-like peptide - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #ext_change 15-Jun-2001
C/Accession: A33802
R/Cockle, S.M.; Aitken, A.; Beg, F.; Smyth, D.G.
J. Biol. Chem. 264, 7788-7791, 1989
A/Title: A novel peptide, pyroglutamylglutamyproline amide, in the rabbit prostate com
A/Reference number: A33802; PMID:89255196; PMID:2498305
A/Accession: A33802
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-3 <COC>
C/Superfamily: unassigned animal peptides
C/Keywords: amidated carboxyl end; pyroglutamic acid
F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 60.0%; Score 12; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EP 4
DB 2 EP 3

RESULT 2

I51049
metallothionein-A - rainbow trout (fragment)
C/Species: Oncorhynchus mykiss (rainbow trout)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #ext_change 21-Jul-2000
C/Accession: I51049
R/Olsson, P.E.; Kling, P.; Ertel, L.J.; Kille, P.
Eur. J. Biochem. 230, 344-349, 1995
A/Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) m
A/Reference number: I51049; PMID:95324545; PMID:7601121
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-4 <OUS>
A/Cross-references: EMBL:X80181; NID:g1019799; PIDN:CA56466.1; PID:g4379328

Query Match 55.0%; Score 11; DB 2; Length 4;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
DB 1 MDP 3

RESULT 3
E44823
synaptosomal-associated protein SNAP-25 peptide 1 - rabbit (fragment)
N/Alternate names: superprotein peptide 1
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C/Accession: E44823
R/Owner: A.; Liu, W.S.; Baltinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A/Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
A/Reference number: A44823; MUID:92044785; PMID:1941090
A/Accession: E44823
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-4 <LOB>
A/Experimental source: visual tissue
A/Note: sequence extracted from NCBI backbone (NCBIP:64247)
C/Keywords: membrane trafficking

Query Match
Best Local Similarity 50.0%; Score 10; DB 2; Length 4;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
DB 1 IME 3

RESULT 4
A02147
phagocytosis-stimulating peptide (tuftsin) - human
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 03-Feb-1994
C/Accession: A02147
R/Mishloka, K.; Constantinopolous, A.; Satch, P.S.; Najjar, V.A.
Biochem. Biophys. Res. Commun. 47, 172-179, 1972
A/Title: The characteristics, isolation and synthesis of the phagocytosis stimulating pe
A/Reference number: A02147; MUID:72187087; PMID:4112769
A/Accession: A02147
A/Residues: 1-4 <NIS>
A/Molecule type: protein
A/Note: a peptide having the same structure, physical properties, and biological activit
R/Fidalgo, B.V.; Najjar, V.A.
Biochemistry 6, 3386-3392, 1967
A/Reference number: A37502; MUID:68091045; PMID:4169272
A/Contents: annotation; immunoglobulin class
C/Comment: An IgG (called leucokinin) binds reversibly to the cell membrane of neutrophil
n is essential for maximum stimulation of the phagocytic activity of neutrophils.
C/Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match
Best Local Similarity 40.0%; Score 8; DB 2; Length 4;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EP 4
DB 2 KP 3

RESULT 5
RHMDTO
thyroliberin - Bombina orientalis
C/Species: Bombina orientalis
C/Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C/Accession: A90919; A01415
R/Yasuhara, T.; Nakajima, T.
Chem. Pharm. Bull. 23, 3301-3303, 1975
A/Title: Occurrence of Pyl-His-Pro-NH₂ in the frog skin.
A/Reference number: A90919; MUID:76138399; PMID:815011
A/Accession: A90919
A/Molecule type: protein
A/Residues: 1-3 <YAS>

C/Superfamily: thyroliberin precursor
C/Keywords: amidated carboxyl end; cutaneous gland; hormone; pyroglutamic acid
F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match
Best Local Similarity 35.0%; Score 7; DB 3; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
DB 3 P 3

RESULT 6
RHRCST
thyroliberin - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C/Accession: A01415
R/Mair, R.M.G.; Barrett, J.F.; Bowers, C.Y.; Schally, A.V.
Biochemistry 9, 1103-1106, 1970
A/Title: Structure of porcine thyrotropin releasing hormone.
A/Reference number: A90560; MUID:70136150; PMID:4584938
A/Accession: A01415
A/Molecule type: protein
A/Residues: 1-3 <NAI>
R/Boler, J.; Enzmann, F.; Folkers, K.; Bowers, C.Y.; Schally, A.V.
Biochem. Biophys. Res. Commun. 37, 705-710, 1969
A/Title: The identity of chemical and hormonal properties of the thyrotropin releasing i
A/Reference number: A90167; MUID:70039904; PMID:4982117
A/Contents: annotation
A/Note: biological activities and Rf values (in 17 chromatographic systems) of the synti
C/Superfamily: thyroliberin precursor
C/Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match
Best Local Similarity 35.0%; Score 7; DB 3; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
DB 3 P 3

RESULT 7
RHSHRT
thyroliberin - sheep
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C/Accession: A93750; A01415
R/Desiderio Jr., D.M.; Burgess, R.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.
Org. Mass Spectrom. 5, 221-228, 1971
A/Title: The elucidation of the primary structure of the hypothalamic thyroid stimulat
A/Reference number: A93750
A/Accession: A93750
A/Molecule type: protein
A/Residues: 1-3 <DES>
R/Burgus, R.; Dunn, T.F.; Desiderio, D.; Ward, D.N.; Vale, W.; Guillemin, R.
Nature 226, 321-325, 1970
A/Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.
A/Reference number: A93161; MUID:70163386; PMID:4585794
A/Contents: annotation
A/Note: physicochemical characteristics and biological activities of the natural and sy
C/Superfamily: thyroliberin precursor
C/Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match
Best Local Similarity 35.0%; Score 7; DB 3; Length 3;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 P 4
|
Db 3 P 3

RESULT 8

A92971
thyroliberin - eastern newt (tentative sequence)
C:Species: Notopterus viridescens; Triturus viridescens (eastern newt)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A92971; A01415
R:Grimm-Jorgensen, Y.; McKelvy, J.F.
J. Neurochem. 23, 471-478, 1974
A:Title: Biosynthesis of thyroliberin releasing factor by newt (Triturus viridescens) bra
A:Reference number: A92971; PMID:75035605; PMID:4214528
A:Accession: A92971
A:Molecule type: protein
A:Residues: 1-3 <GR>
A:Note: a peptide with the chromatographic and electrophoretic characteristics of thyro
lutidine, or glutamic acid
C:Superfamily: thyroliberin precursor
C:Keywords: amidated carboxyl end; cutaneous gland; hormone; hypothalamus; pyroglutamic
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 35.0%; Score 7; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
|
Db 3 P 3

RESULT 9

A43391
TRH-like tripeptide - alfalfa
C:Species: Medicago sativa (alfalfa)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A43391
R:Backey, D.B.
J. Biol. Chem. 267, 17508-17511, 1992
A:Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroglu-
A:Reference number: A43391; PMID:92388032; PMID:1517203
A:Accession: A43391
A:Molecule type: protein
A:Residues: 1-3 <LAC>
C:Keywords: amidated carboxyl end; pyroglutamic acid (Gln) #status experimental
F:1/Modified site: pyrrolidone carboxylic acid (Pro) #status experimental
F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 35.0%; Score 7; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
|
Db 3 P 3

RESULT 10

I78890
tyrosine protein kinase - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: I78890
R:Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C.
Oncogene 9, 3437-3448, 1994
A:Title: Two distinct protein isoforms are encoded by ntck, a csk-related tyrosine protei
A:Reference number: I58407; PMID:95060800; PMID:7970703
A:Accession: I78890

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3 <RES>
A:Cross-references: GB:I33339; NID:G609536; PIDN:AAA64432.1; PID:G609538
C:Genetics:
A:Gene: p52nck

Query Match 35.0%; Score 7; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
|
Db 2 P 2

RESULT 11

A32039
tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
C:Accession: A32039
R:Horvath, A.; Kastin, A.J.
J. Biol. Chem. 264, 2175-2179, 1989
A:Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor
A:Reference number: A32039; PMID:89123285; PMID:2563371
A:Accession: A32039
A:Molecule type: protein
A:Residues: 1-4 <HOR>
A:Experimental source: brain
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end
F:4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 35.0%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
|
Db 2 P 2

RESULT 12

PL0140
carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydohydrogen
C:Species: Pseudomonas carboxydohydrogena
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
C:Accession: PL0140
R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
Arch. Microbiol. 152, 335-341, 1989
A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotro
A:Reference number: PL0138; PMID:90055678; PMID:2818128
A:Accession: PL0140
A:Molecule type: protein
A:Residues: 1-4 <KRA>
C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, m
C:Keywords: oxidoreductase

Query Match 35.0%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
|
Db 4 P 4

RESULT 13

A61300
22k superhelical DNA-binding protein - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999

C:Accession: A61300
 R:Kishi, F.; Ebina, Y.; Miki, T.; Nakazawa, T.; Nakazawa, A.
 J. Biochem. 92, 1059-1068, 1982
 A:Title: Purification and characterization of a protein from *Escherichia coli* which forms a dodecamer
 A:Reference number: A61300; MUID:93082696; PMID:6294066
 A:Accession: A61300
 A:Molecule type: protein
 A:Residues: 1-4 <KIS>
 C:Comment: This protein resembles some of the histone-like proteins of bacteria in amino acid composition and DNA binding; monomer

Query Match 35.0%; Score 7; DB 2; Length 4;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LE 3
 : |
 Db 1 ME 2

RESULT 14

157745
 D-mannanase hydrolase (uxuA) - *Escherichia coli*
 C:Species: *Escherichia coli*
 C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 08-Oct-1999
 C:Accession: 157745
 R:Blanco, C.; Ritzenhauer, P.; Kolb, A.
 Mol. Gen. Genet. 202, 112-119, 1986
 A:Title: The regulatory region of the *uxuA* operon in *Escherichia coli* K12.
 A:Reference number: 157745; MUID:66174344; PMID:3083215
 A:Accession: 157745
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-4 <RES>
 A:Cross-references: EMBL:X03411; NID:943300; PIDN:CAA27147.1; PID:9581254

Query Match 35.0%; Score 7; DB 2; Length 4;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LE 3
 : |
 Db 1 ME 2

RESULT 15

S53508
 starvation-induced ribonuclease - tomato
 C:Species: *Lycopersicon esculentum* (tomato)
 C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
 C:Accession: S53508
 R:Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.
 Plant Mol. Biol. 27, 477-485, 1995
 A:Title: cDNA structure and regulatory properties of a family of starvation-induced ribonucleases
 A:Reference number: S53506; MUID:95201242; PMID:7894013
 A:Accession: S53508
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-4 <KOE>

Query Match 35.0%; Score 7; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
 : |
 Db 2 P 2

Search completed: November 25, 2003, 14:08:22
 Job time : 21 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 14:01:32 ; Search time 11 Seconds
(without alignments)
17.101 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20
Sequence: 1 VLEP 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 18

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	40.0	4	1 TUFT_HUMAN	P01858 homo sapien
2	7	35.0	3	1 THYL_PIG	P01151 sus scrofa
3	7	35.0	4	1 DCM1_PSECH	P19916 pseudomonas
4	7	35.0	4	1 RMO1_YEAST	P36515 saccharomyc
5	5	25.0	4	1 EOS1_HUMAN	P02271 homo sapien
6	4	20.0	4	1 PAR3_HIRME	P42562 hirudo medi
7	4	20.0	4	1 FLRF_HIRME	P42561 hirudo medi
8	4	20.0	4	1 FLRN_VIBFI	P58707 antioptleura
9	3	15.0	3	1 LUXE_VIBFI	P24272 vibrio fisc
10	3	15.0	4	1 FYRI_ANTEU	P58706 antioptleura
11	2	10.0	4	1 ACHI_ACHFU	P35904 achartina fu
12	2	10.0	4	1 DCM5_PSECH	P19918 pseudomonas
13	2	10.0	4	1 PAR4_HIRME	P42563 hirudo medi
14	2	10.0	4	1 FMRF_MACNI	P01162 macrocallis
15	2	10.0	4	1 OCPI_OCTMI	P58648 octopus min
16	2	10.0	4	1 OCPI_OCTMI	P58649 octopus min
17	1	5.0	3	1 GRNM_HUMAN	P01157 homo sapien
18	1	5.0	4	1 FFKA_ANTEU	P58705 antioptleura

ALIGNMENTS

RESULT 1
TUFT_HUMAN STANDARD; PRT; 4 AA.
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phagocytosis-stimulating peptide (Tuftsin).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=72187087; PubMed=4112769;
RX Nishioka K., Constantinopoulos A., Satoh P.S., Najjar V.A.;
RT "The characteristics, isolation and synthesis of the phagocytosis
stimulating peptide tuftsin."
RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
RN [2]
RP IMMUNOGLOBULIN CLASS.
RX MEDLINE=68091045; PubMed=4169272;
RX Fidalgo B.V., Najjar V.A.;
RT "The physiological role of the lymphoid system. VI. The stimulatory
effect of leucophilic gamma globulin (leucokinin) on the phagocytic
activity of human polymorphonuclear leucocyte."
RL Biochemistry 6:3386-3392(1967).
CC -1- MISCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE
CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININSE ON THE
MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.
CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC
CC ACTIVITY OF NEUTROPHILS.
DR PIR; A02147; A02147.
DR MIM; 191150; -.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006909; P:phagocytosis; NAS.
SQ SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;
Query Match 40.0%; Score 8; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 EP 4
Db 2 KP 3
RESULT 2
THYL_PIG STANDARD; PRT; 3 AA.
ID THYL_PIG
AC P01151;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thylolipin (Thyrotropin releasing hormone) (TRH) (Protrelinin).
OS Sus scrofa (Pig).
OS Ovis aries (Sheep).
OS Bombina orientalis (Oriental fire-bellied toad), and
OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sue.
OX NCBI_TaxID=9823; 9940; 8346; 8316;
RN [1]
RP SEQUENCE.
RX SPECIES=Pig; TISSUE=Hypothalamus;
RX MEDLINE=70136150; PubMed=4984938;
RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
RT "Structure of porcine thyrotropin releasing hormone."
RL Biochemistry 9:1103-1106(1970).
RN [2]
RP SYNTHESIS.
RX SPECIES=Pig;
RX MEDLINE=70039904; PubMed=4982117;
RX Bolter U., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
RT "The identity of chemical and hormonal properties of the thyrotropin
releasing hormone and pyroglutamyl-histidyl-proline amide."
RL Biochem. Biophys. Res. Commun. 37:705-710(1969).
RN [3]
RP SEQUENCE.
RX SPECIES=Sheep; TISSUE=Hypothalamus;
RX Desiderio D.M. Jr., Burgess R., Dunn T.F., Vale W., Guillemin R.,
Ward D.N.;
RT "The elucidation of the primary structure of the hypothalamic thyroid

RT stimulating hormone releasing factor of ovine origin by means of mass
 RT spectrometry.";
 RL Ory. Mass Spectrom. 5:221-228(1971).
 RN (4)
 RP SYNTHESIS.
 RC SPECIES=Sheep;
 RX MEDLINE=7016336; PubMed=4985794;
 RA Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
 RT "Characterization of ovine hypothalamic hypophysiotropic
 TSH-releasing factor.";
 RL Nature 226:321-325(1970).
 RN (5)
 RP SEQUENCE.
 RC SPECIES=B.orientalis; TISSUE=Skin;
 RX MEDLINE=7613839; PubMed=815011;
 RA Yasuhara T., Nakajima T.;
 RT "Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
 RL Chem. Pharm. Bull. 23:3301-3303(1975).
 RN (6)
 RP SEQUENCE.
 RC SPECIES=N.viridescens;
 RX MEDLINE=7503560; PubMed=4214528;
 RA Grimm-Joergensen Y., McKelvy J.F.;
 RT "Bioynthesis of thyrotropin releasing factor by newt (Triturus
 viridescens) brain in vitro. Isolation and characterization of
 thyrotropin releasing factor.";
 RL J. Neurochem. 23:471-478(1974).
 CC -1- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH
 IN THE ANTERIOR PITUITARY GLAND AND AS A NEUOTRANSMITTER/
 CC NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.
 DR PIR: A90919; RHRDIO.
 DR PIR: A92971; A92971.
 DR PIR: A93750; RSHST.
 KW Amidation; Pyroglutamate carboxylic acid.
 FT MOD_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.
 FT MOD_RES 3 3 AMIDATION.
 SQ SEQUENCE 3 AA; 380 MW; 7761FEB000000000 CRC64;
 Query Match 35.0%; Score 7; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 P 4
 Db 3 P 3
 RESULT 3
 DCML_PSECH STANDARD; PRT; 4 AA.
 ID DCML_PSECH
 AC P19916;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
 dehydrogenase subunit L) (CO-DH L) (Fragment).
 GN COTL.
 OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae.
 OX NCBI_TaxID=290;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hengstler I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydohydrogenic bacteria.";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 dioxide.
 CC -1- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 acceptor.

CC -1- COFACTOR: Molybdenum (molybdopterin).
 CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR: P10140; P10140.
 KW Oxidoreductase; Molybdenum.
 FT NON_TER 4
 SQ SEQUENCE 4 AA; 441 MW; 7761E876F000000000 CRC64;
 Query Match 35.0%; Score 7; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 P 4
 Db 4 P 4
 RESULT 4
 RM01_YEAST STANDARD; PRT; 4 AA.
 ID RM01_YEAST
 AC P36515;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Mitochondrial 60S ribosomal protein L1 (Yml1) (Fragment).
 GN MRPL.
 OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=91285106; PubMed=2060626;
 RA Grohmann L., Graack H.-R., Krufe V., Choli T., Goldschmidt-Reisin S.,
 RA Kitakawa M.;
 RT "Extended N-terminal sequencing of proteins of the large ribosomal
 RT subunit from yeast mitochondria.";
 RL FEBS Lett. 284:51-56(1991).
 DR PIR: S17255; S17255.
 DR SCD; L0002681; MRPL.
 DR Ribosomal protein; Mitochondrion.
 KW NON_TER 4
 FT NON_TER 4
 SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D000000000 CRC64;
 Query Match 35.0%; Score 7; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 P 4
 Db 4 P 4
 RESULT 5
 E0S1_HUMAN STANDARD; PRT; 4 AA.
 ID E0S1_HUMAN
 AC P02731;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DE Eosinophilic leucocyte peptides.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=76078412; PubMed=1060093;
 RA Goetzl E.J., Austen K.F.;
 RT "Purification and synthesis of eosinophilic tetrapeptides of
 RT human lung tissue: Identification as eosinophil chemotactic factor of
 RT anaphylaxis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).

CC -1- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG
 (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS
 (ANAPHYLAXIS). THEIR ACTIVITIES, PREPARENTIALLY AFFECTING
 EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE
 OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
 DR GO:0030105; P:anaphylaxis; IDA.
 DR GO:0006935; P:chemotaxis; IDA.
 FT VARIANT 1
 V -> A (IN OTHER PEPTIDE).
 /FTID=VAR.005201.
 SQ SEQUENCE 4 AA; 390 MW; 6805862A00000000 CRC64;
 Query Match 25.0%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred.No.1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 E 3
 Db 4 E 4
 RESULT 6
 FARP_HIRME STANDARD; PRT; 4 AA.
 ID FARP3_HIRME
 AC P42562;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE FMRFamide-like neuropeptide YLRf-amide.
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;
 CC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
 NCBI_TaxID=6421;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Katsoris M.A., Calabrese R.L.;
 RT "Identification of Rfamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 FT MOD_RES 4
 FT MOD_RES 4
 SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;
 Query Match 20.0%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred.No.1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 L 2
 Db 2 L 2
 RESULT 7
 FLRF_HIRME STANDARD; PRT; 4 AA.
 ID FLRF_HIRME
 AC P42561;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE FLRFamide.
 OS Hirudo medicinalis (Medicinal leech), and
 OS Helisoma trivolvis (Snail)
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;
 CC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
 NCBI_TaxID=6421, 27815;
 RN (1)
 RP SEQUENCE.
 RC SPECIES=H. medicinalis;
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans B.D., Pohl J., Katsoris M.A., Calabrese R.L.;
 RT "Identification of Rfamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).

RN [2]
 RP SEQUENCE.
 RC SPECIES=H. trivolvis; TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
 trivolvis.";
 RL Peptides 15:31-36(1994).
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 FT MOD_RES 4
 FT MOD_RES 4
 SQ SEQUENCE 4 AA; 582 MW; 69D40729A00000000 CRC64;
 Query Match 20.0%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred.No.1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 L 2
 Db 2 L 2
 RESULT 8
 FLRN_ANTELL STANDARD; PRT; 4 AA.
 ID FLRN_ANTELL
 AC P58707;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Antho-RNamide.
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthaeae; Actiniidae; Anthopleura.
 NCBI_TaxID=6110;
 RN (1)
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RX MEDLINE=90319122; PubMed=1973541;
 RA Grimmett-Khiujzen C.J.P., Rinehart K.L., Jr., Jacob E., Graff D.,
 RA Reinscheid R.K., Notack H.-P., Staley A.L.;
 RT "Isolation of L-3-phenylacetyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
 anemone neuropeptide containing an unusual amino-terminal blocking
 group.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Neuron-specific.
 CC -1- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.
 DR PIR; A35779; A35779.
 CC Neuropeptide; Amidation.
 FT MOD_RES 1
 FT MOD_RES 4
 FT MOD_RES 1
 SQ SEQUENCE 4 AA; 549 MW; 64540729A00000000 CRC64;
 Query Match 20.0%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred.No.1.3e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 L 2
 Db 2 L 2
 RESULT 9
 LUXE_VIBFI STANDARD; PRT; 3 AA.
 ID LUXE_VIBFI
 AC P24272;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) (Acyl-
 DE protein synthetase) (Fragment).
 GN LUXE.
 OS Vibrio fischeri.

```

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=668;
RP [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91072226; PubMed=2254256;
RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
RT "A new Vibrio fischeri lux gene precedes a bidirectional termination
site for the lux operon."
RL J. Bacteriol. 172:6797-6802(1990).
CC -1- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
CC IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
CC FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
CC SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
CC -1- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
CC an acyl-protein thioester.
CC -1- PATHWAY: Bioluminescent fatty acid reduction system; second step.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M62812; -; NOT_ANNOTATED_CDS.
KM Luminescence; Ligase.
FT NON_TER 1
SQ SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;

Query Match 15.0%; Score 3; DB 1; Length 3;
Best Local Similarity 0.0%; Pred. No. 1.3e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 V 1
Db 1 I 1

RESULT 10
PYRI_AMEL
ID PYRI_AMEL STANDARD; PRT; 4 AA.
AC P58706;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antho-Riamide I [Contains: Antho-Riamide II].
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
OC Nynantheae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=92270459; PubMed=1821096;
RA Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
RA Grimmelikhuijzen C.J.P.;
RT "Isolation of two novel neuropeptides from sea anemones: the unusual,
RT biologically active L-3-phenylalanyl-Tyr-Arg-Ile-NH2 and its
RT des-phenylalanyl fragment Tyr-Arg-Ile-NH2."
RL Peptides 12:1165-1173(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-Riamide and Antho-Riamide II."
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron-specific.

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KM Neuropeptide; Amidation.
FT CHAIN 1 4 ANTHO-RIAMIDE I.
FT CHAIN 2 4 ANTHO-RIAMIDE II.
FT MOD_RES 1 1 L-3-PHENYLALACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;

Query Match 15.0%; Score 3; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 1.3e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 V 1
Db 4 I 4

RESULT 11
ACH1_ACHFU
ID ACH1_ACHFU STANDARD; PRT; 4 AA.
AC P35904;
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Achatina fulica (giant African snail).
OS Achatina fulica (giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigamurethra; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RC STRAIN=Perussac; TISSUE=Ganglion;
RX MEDLINE=91264856; PubMed=1675568;
RA Kametani Y., Minakata H., Kenny P.T.M., Iwashita T., Matanabe K.,
RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.,
RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
RT fulica Ferussac containing a D-amino acid residue."
RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN [2]
RP CHARACTERIZATION.
RC STRAIN=Perussac; TISSUE=Heart atrium;
RX MEDLINE=91264856; PubMed=1675568;
RA Fujimoto K., Kubota I., Yasuda-Kametani Y., Minakata H., Nomoto K.,
RA Yoshida M., Harada A., Muneka Y., Kobayashi M.;
RT "Purification of achatin-I from the atria of the African giant snail,
RT Achatina fulica, and its possible function."
RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=93014529; PubMed=1399265;
RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kametani Y., Minakata H.,
RA Iwashita T., Nomoto K.;
RT "Crystal structure and molecular conformation of achatin-I
RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
RT D-amino acid residue."
RL Int. J. Pept. Protein Res. 39:258-264(1992).
CC -1- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
CC AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
CC NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
CC HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
CC PIR: A32480; A32480.
KM Hormone; D-amino acid.
FT MOD_RES 2 2 D-PHENYLLALANINE.
SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match 10.0%; Score 2; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 1.3e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 E 3
Db 4 D 4

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RESULT 12
DCMS_PSECH STANDARD; PRT; 4 AA.
ID DCMS_PSECH
AC P19918;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO
dehydrogenase subunit S) (CO-DH S) (Fragment).
GN CUTS.
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1];
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
carboxydohydrogenic bacteria."
RL Arch. Microbiol. 152:335-341(1989).
CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
dioxide.
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
acceptor.
CC -1- COFACTOR: BINDS TWO 2FE-2S CLUSTERS.
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
SMALL.
DR PIR; P10146; P10146.
KW Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe-2S.
FT NON TER
SQ SEQUENCE 4 AA; 420 MW; 6DD33D6F00000000 CRC64;

Query Match 10.0%; Score 2; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 1.3e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 L 2
DB 1 M 1

RESULT 13
FAR4_HIRME STANDARD; PRT; 4 AA.
ID FAR4_HIRME
AC P42563;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide YMRP-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudindae; Hirudo.
OX NCBI_TaxID=6421;
RN [1];
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamde neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES
SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match 10.0%; Score 2; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 1.3e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 L 2
DB 2 M 2

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DB 2 M 2

RESULT 14
FMRF_MACNT STANDARD; PRT; 4 AA.
ID FMRF_MACNT
AC P01162;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE FMRFamide (Peak C) (Cardioexcitatory neuropeptide).
OS Macrocallista nimbosa (Sun-ray clam),
OS Nereis virens (Sandworm),
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
OC Veneroidea; Veneridae; Macrocallista.
OX NCBI_TaxID=6594, 6353, 6421, 27815;
RN [1];
RP SEQUENCE, AND SYNTHESIS.
RX SPECIES=M.nimbosa; TISSUE=Cerebral pedal, and Visceral ganglion;
RX MEDLINE=77715956; PubMed=877582;
RA Price D.A., Greenberg M.J.;
RT "Structure of a molluscan cardioexcitatory neuropeptide."
RL Science 197:670-671(1977).
RN [2];
RP SEQUENCE, AND CHARACTERIZATION.
RX SPECIES=M.nimbosa; TISSUE=ganglion;
RX MEDLINE=78012038; PubMed=909875;
RA Price D.A., Greenberg M.J.;
RT "Purification and characterization of a cardioexcitatory neuropeptide
from the central ganglia of a bivalve mollusc."
RL Prep. Biochem. 7:261-281(1977).
RN [3];
RP SEQUENCE.
RX SPECIES=N.virens;
RX MEDLINE=90259866; PubMed=2342992;
RA Krajinak K.G., Price D.A.;
RT "Authentic FMRFamide is present in the polychaete Nereis virens.";
RL Peptides 11:75-77(1990).
RN [4];
RP SEQUENCE.
RX SPECIES=H.medicalialis;
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamde neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
RN [5];
RP SEQUENCE.
RX SPECIES=H.trivolvis; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
trivolvis."
RL Peptides 15:31-36(1994).
CC -1- FUNCTION: MYOACTIVE; CARDIOEXCITATORY SUBSTANCE. PHARMACOLOGICAL
ACTIVITIES INCLUDE AUGMENTATION, INDUCTION, AND REGULARIZATION OF
CARDIAC CONTRACTION.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
DR PIR; A01426; ECNK.
KW Neuropeptide; Amidation.
FT MOD RES
SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;

Query Match 10.0%; Score 2; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 1.3e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 L 2
DB 2 M 2

```

RESULT 15

OCPI_OCTMI STANDARD; PRT; 4 AA.
 AC P58648;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cardioactive peptides Ocp-1/Ocp-2.
 OS Octopus minor (Octopus).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
 OX NCBI_TaxID=89766;
 RN [1]
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
 RC TISSUE=Brain;
 RX MEDLINE=20336815; Pubmed=10876044;
 RA Iwakoshi E., Hisada M., Minakata H.;
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
 RT Octopus minor".
 RL Peptides 21:623-630(2000).
 CC -1- FUNCTION: Cardioactive; has both positive chronotropic and
 CC inotropic effects on the heart. Ocp-2 is a 1000 time less
 CC active than Ocp-1.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: Ocp-2 has L-Phe instead of D-Phe.
 CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
 KW Hormone; D-amino acid.
 FT MOD_RES 2
 FT D-PHENYLALANINE.
 SQ SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;

Query Match 10.0%; Score 2; DB 1; Length 4;
 Best Local Similarity 0.0%; Pred.No. 1.3e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 E 3
 :
 Db 4 D 4

Search completed: November 25, 2003, 14:07:03
 Job time : 12 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 14:04:37 ; Search time 34 Seconds
(without alignments)
30.359 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20
Sequence: 1 VLEP 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp Unclassified:*
- 15: sp_rvrius:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	45.0	4	Q08433	rattus sp.

ALIGNMENTS

RESULT 1

Q08433 PRELIMINARY; PRT; 4 AA.

AC Q08433; 01-NOV-1996 (T-EMBLrel. 01, Created)

DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)

DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)

DE Bilirubin UDP-glucuronosyltransferase (Fragment).

OS Rattus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10118;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Gun;

RX MEDLINE=91282758; PubMed=1840486;

RA Sato H., Aono S., Kaishiwamata S., Koiwai O.,

RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the

RL hyperbilirubinemic Gunn rat." ;

DR Biochem. Biophys. Res. Commun. 177:1161-1164(1991).

EMBL: S38636; AAB19259.1; -.

KW Bilirubin UDP-glucuronosyltransferase.

FT NON TER 1 1

SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 45.0%; Score 9; DB 11; Length 4;
Best Local Similarity 66.7%; Pred. No. 8.3e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLE 3
Db 2 VLK 4

Search completed: November 25, 2003, 14:07:49
Job time : 35 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 14:00:57 ; Search time 41 Seconds
(without alignments)
15.486 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20
Sequence: 1 VLEP 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 13293

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*

8: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*

10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*

11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*

12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*

13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*

14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*

16: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*

17: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*

18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*

19: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*

20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*

22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	4	21	Chemotactic peptid
2	20	100.0	4	22	Adhesion-modulator
3	20	100.0	4	24	Macrophage recruit
4	16	80.0	4	20	Interleukin-1 beta
5	14	70.0	4	20	Peptide used to ma
6	14	70.0	4	21	Chemotactic peptid
7	14	70.0	4	21	Granzyme B substra
8	14	70.0	4	21	Granzyme-B substra
9	14	70.0	4	21	Fluorophore-label1

10	14	70.0	4	22	AAU79766	Chicken bone deriv
11	14	70.0	4	22	AAB82937	Granzyme B peptide
12	14	70.0	4	22	AAG62561	Cresyl violet subs
13	14	70.0	4	22	AAB29759	Escherichia coli r
14	14	70.0	4	23	AAB28993	Human thrombin cle
15	14	70.0	4	23	ABG94471	Protease biosensor
16	14	70.0	4	23	AAE19128	Granzyme B peptide
17	14	70.0	4	23	AAAM50406	Tumour associated
18	14	70.0	4	23	AAAM50407	Tumour associated
19	14	70.0	4	23	AAAM50466	Tumour associated
20	14	70.0	4	23	AAAM50470	Tumour associated
21	14	70.0	4	23	AAAM50471	Tumour associated
22	13	65.0	4	8	AAAP71434	Immunomodulator pe
23	13	65.0	4	13	AAAR3726	ACE inhibitor pept
24	13	65.0	4	16	AAAG3983	Antineoplastic pep
25	13	65.0	4	19	AAAM62052	Human erythropoiet
26	13	65.0	4	20	AAI15644	Peptide used to ma
27	13	65.0	4	20	AAAM83445	Human growth hormo
28	13	65.0	4	21	AAAG80808	Fluorophore-label1
29	13	65.0	4	21	AAAG61373	Cadherin-7 cell ad
30	13	65.0	4	22	AAU79767	Chicken bone deriv
31	13	65.0	4	22	AAAB30764	Peptide which is u
32	13	65.0	4	23	ABG61371	Tick Ixolais firs
33	12	60.0	2	22	AAAB91036	Thyrotropin releas
34	12	60.0	2	24	ABU06374	Maize starch synth
35	12	60.0	3	16	AAAR3188	Tripeptide having
36	12	60.0	3	19	AAAM6205	Anti-inflammatory
37	12	60.0	3	21	AAAG6894	Peptide used as an
38	12	60.0	4	5	AAAP40420	Animal growth prom
39	12	60.0	4	5	AAAP40424	Acetylcholinestera
40	12	60.0	4	9	AAAP82910	Sequence of peptid
41	12	60.0	4	9	AAAP80424	Diuretic hormone b
42	12	60.0	4	14	AAAR38100	Diuretic hormone b
43	12	60.0	4	14	AAAR38441	Diuretic hormone b
44	12	60.0	4	14	AAAR42094	Diuretic hormone d
45	12	60.0	4	14	AAAR42095	Diuretic hormone d

ALIGNMENTS

RESULT 1	
ID	AAB28663
	AAB28663 standard; peptide; 4 AA.
AC	AAB28663;
XX	
DT	13-FEB-2001 (first entry)
XX	
DE	Chemotactic peptide pepd'.
XX	
KW	Chemotactic; osteopontin; vulnery; antiarthritic; antipsoriatic;
KW	cytostatic; antitumor; antinflammatory; osteopathic;
KW	wound healing; cell migration; chemotaxis; atherosclerosis; cancer;
KW	angiogenic-associated disease; arthritis; psoriasis; haemangioma;
KW	ocular neovascularisation; cell apoptosis; nitrous oxide production;
KW	inflammation; osteoporosis; immune disease.
OS	Mammalia.
OS	Synthetic.
XX	
PN	WO200063247-A2.
XX	
PD	26-OCT-2000.
XX	
PF	17-APR-2000; 2000WO-US10344.
XX	
PR	15-APR-1999; 99US-0129764.
XX	
PA	(CHIL-) CHILDRENS MEDICAL CENT.
XX	
PI	Ashkar S;
XX	

DR WPI; 2000-687159/67.

XX New osteopontin-derived chemotactic and inhibitory peptides, useful for
PT promoting scarless wound healing, modulating cellular chemotaxis,
PT treating formation of atherosclerotic plaques and preventing metastasis

XX Claim 17; Page 43; 54pp; English.

XX The present sequence is an osteopontin-derived chemotactic peptide.
CC Such chemotactic peptides are useful for promoting scarless wound
CC healing, modulating chemotaxis and promoting cell migration to a target
CC site in a cell of a subject. They are also used for modulating cellular
CC chemotaxis in a mammalian cell such as smooth muscle cell, a macrophage,
CC an endothelial cell, a vascular cell and a tumorigenic cell. They are
CC useful for treating the formation of atherosclerotic plaques in a
CC subject. The peptides are used for preventing metastasis, treating an
CC angiogenic-associated disease such as arthritis, psoriasis, haemangioma,
CC tumour metastasis or ocular neovascularisation. They are also used for
CC activating cell apoptosis, for modulating nitrous oxide production and
CC for inducing chemotaxis. The peptides are useful for diagnosing, treating
CC and preventing tumour metastasis, inflammation, osteoporosis and immune
CC diseases. They can also be used to enhance an immune response by
CC attracting macrophages.

XX Sequence 4 AA;

Query Match 100.0%; Score 20; DB 21; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
1 VLEP 4

DB 1 VLEP 4

RESULT 2

AB29558 AAB29558 standard; peptide; 4 AA.

XX AAB29558;

DT 14-FEB-2001 (first entry)

DE Adhesion-modulatory peptide, SEQ ID NO:15.

XX Adhesion modulatory peptide; target cell adhesion; cell adhesion;
KW endothelial cell; fibroblast; macrophage; neutrophil; myofibroblast;
KW collagen; glycosaminoglycan; extracellular matrix; synthetic substrate;
KW vascular growth; wound healing; keloid formation; scarring; fibrosis;
KW anticoagulant; vulnery; immunomodulatory; antibacterial; anticancer;
XX anti-tumorigenic; anti-CD4 activity; prosthesis; implant.

XX Synthetic.

PN WO200063236-A2.

PD 26-OCT-2000.

PF 17-APR-2000; 2000MO-US10329.

PR 16-APR-1999; 99US-0129709.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PI Ashkar S;

XX WPI; 2001-007002/01.

PT Novel adhesive modulatory peptides useful for modulating adhesion of
PT target cells such as endothelial cells, fibroblasts, macrophages to
PT substrate such as polyvinyl surfaces, collagen

PS Claim 8; Page 27; 35pp; English.

XX The invention relates to novel adhesion modulatory peptides (AAB29544-
CC AAB29558) which modulate the adhesion of a target cell to a substrate.
CC The invention also encompasses substrates and devices treated with a
CC peptide of the invention; compositions comprising a peptide of the
CC invention for in vivo use; and analogues, fragments and chemical
CC derivatives of the peptide of the invention. The peptides are useful for
CC modulating the adhesion to a substrate of target cells such as
CC endothelial cells, fibroblasts, macrophages, neutrophils or
CC myofibroblasts. The substrate may be a substrate that is found in the
CC body of a patient, e.g., collagen or hyaluronic acid, or may be a
CC synthetic substrate e.g., a polyvinyl surface, titanium or PGA. The
CC peptides are useful for regulating vessel growth during wound healing
CC and/or in the treatment of damage resulting from vascular disease; for
CC inhibiting or preventing cellular apoptosis; in the treatment of
CC fibrosis, in particular in the clearing of debris; to minimise wound
CC contraction, thereby reducing keloid tissue formation and scarring; and
CC as anti clotting agents. The peptides also have an immunomodulatory
CC effect, and an antibacterial effect by adhering to neutrophils.
CC Additionally, peptides of the invention have an anticancer effect by
CC competing for alpha-v-beta3 integrin binding on the cell surface, and an
CC anti-tumorigenic effect by having anti-CD4 activity. The peptides are
CC useful for stimulating and/or enhancing cell attachment to polymer
CC scaffolds, to enhance tissue growth and for coating medical devices,
CC including prostheses and implants (e.g., vascular implants). The present
CC sequence represents a specifically claimed adhesion modulatory peptide of
CC the invention.

XX Sequence 4 AA;

Query Match 100.0%; Score 20; DB 22; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
1 VLEP 4

DB 1 VLEP 4

RESULT 3

ABP58757 AAB58757 standard; peptide; 4 AA.

XX AAB58757;

DT 04-APR-2003 (first entry)

DE Macrophage recruitment inhibitor peptide, SEQ ID NO:7.

XX Macrophage recruitment inhibitor peptide; drug discovery; screening;
KW Minicell display; random peptide library; drug discovery; screening;
KW fusion protein; outer membrane protein;
KW Rickettsia rickettsii 17K antigen; bioactive peptide;
KW macrophage recruitment inhibitor; osteopontin; CSA; Fibronectin.

XX Synthetic.

PN WO200272759-A2.

PD 19-SEP-2002.

PF 06-MAR-2002; 2002MO-US06921.

PR 07-MAR-2001; 2001US-274039P.

XX Rickettsia rickettsii 17K antigen; bioactive peptide.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PI Ashkar S;

XX WPI; 2003-046738/04.

PT Minicell display method for screening peptide libraries for peptide

PT candidates that can bind and modulate a particular biological process,
PT comprises identifying minicell hosts bound to the binding partner -
PS Claim 22; Page 36; 66pp; English.

CC The invention relates to minicell display methods for the generation
CC and screening of random peptide libraries for peptide candidates which
CC can bind to and modulate the activity of target molecules involved in
CC biological processes. The methods involve expressing a peptide library as
CC a fusion protein with a bacterial outer membrane protein (preferably the
CC 17K antigen of Rickettsia rickettsii) in an annealed bacterially-derived
CC minicell host, and then contacting the minicell hosts with a target
CC molecule. Minicells comprising a library peptide which has bound to the
CC target molecule are separated from the unbound minicells, and the
CC peptides of interest analysed. The invention also encompasses methods for
CC making a minicell DNA library, increasing the diversity of a minicell DNA
CC library by in vivo mutagenesis, screening a minicell DNA library, and
CC purifying minicells. The methods of the invention are useful for
CC identifying minicell hosts bound to a target molecule and may be used in
CC drug discovery. The method increases the size of the peptides to be
CC screened and the diversification of the library to be screened, thereby
CC increasing the number of potential peptides that can modulate a
CC particular biological response or mechanism. Sequences ABP58757-ABP58803
CC represent bioactive peptides identified using the minicell display
CC method of the invention. The present sequence was characterised as
CC an inhibitor of macrophage recruitment by osteopontin, C5a and
CC fibronectin.

SO Sequence 4 AA;

Query Match 100.0%; Score 20; DB 24; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
|||
1 VLEP 4

RESULT 4
ID AAY03962 standard; peptide; 4 AA.
XX AAY03962;

DT 23-JUN-1999 (first entry)

DE Interleukin-1 beta converting enzyme binding moiety.

XX Cysteine protease inhibitor; oxadiazole; thiazidazole; 1,2,4-triazole;
KM interleukin-1 beta converting enzyme inhibitor; IL-1; ICB; antitumour;
KM anticancer; antimicrobial; antibacterial; antiviral; actinolytic;
KM antiinflammatory; herbicide; fungicide; pesticide; multiple sclerosis;
KM neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KM ischaemic-reperfusion injury.

XX Synthetic.

OS WO9849190-A2.

PN 05-NOV-1998.

PD 24-APR-1998; 98WO-US08259.

PF 23-APR-1998; 98US-0044819.

PR 25-APR-1997; 97US-0044819.

XX (CORT-) CORTECH INC.

XX Cheronis JC, Gerrity JI, Goodfellow VS, Gyorkos AC;

PI Leimer AH, Spruce LW, Young JM;

XX WPI; 1999-131683/11.

XX New substituted oxadiazole cysteine protease inhibitors - useful
PT e.g. for inhibiting cancer cell growth, microbial cell or viral
PT growth or treating inflammatory and degenerative diseases

PS Claims 61, 62; Pages 67, 68; 82pp; English.

CC New compounds are presented which consist of a cysteine protease
CC binding moiety attached by its C-terminal to an oxadiazole, thiazidazole
CC or 1,2,4-triazole moiety. These compounds are cysteine protease
CC inhibitors useful for inhibiting the enzymatic activity of calpain,
CC cathepsin, caspase (e.g. human interleukin-1 beta converting enzyme),
CC viral or microbial cysteine protease (e.g. human coronavirus or
CC gingipain), or protozoan cysteine protease (e.g. Trypanosoma,
CC Schistosoma, Leishmania or Plasmodium protease). They can be used
CC e.g. for: inhibiting cancer cell growth, tumour progression or tumour
CC metastasis; or microbial cell or viral growth (e.g. inhibiting
CC hepatitis A virus 3C proteinase, hepatitis C virus endopeptidase 2,
CC picornain 3C rhinovirus protease, foot and mouth disease virus L
CC proteinase, encephalomyelitis virus endopeptidase 2, picornain 2A
CC protease); treating allergic response symptoms (e.g. inhibiting
CC proenzyme Der p1); treating neurodegenerative disorders (e.g.
CC Alzheimer's disease, Parkinson's disease, multiple sclerosis) and
CC disorders resulting from ischaemic-reperfusion injury (e.g. stroke,
CC myocardial infarction, transplantation, vascular injury or
CC cardiovascular collapse or shock); treating inflammatory and
CC degenerative diseases (e.g. rheumatoid arthritis, osteoarthritis or
CC periodontal disease); or treating pulmonary diseases (e.g. asthma or
CC emphysema). They can also be used for detecting or quantifying cysteine
CC protease activity in a sample, mixture, biological fluid or tissue; for
CC purifying cysteine protease in a sample; or as antibacterial agents,
CC herbicides, fungicides or pesticides.

SO Sequence 4 AA;

Query Match 80.0%; Score 16; DB 20; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
|||
1 LEP 3

RESULT 5
ID AAY15640 standard; Peptide; 4 AA.
XX AAY15640;

DT 27-JUL-1999 (first entry)

DE Peptide used to make fluorescent reporter molecules.

XX Fluorogenic; fluorescent reporter molecule; enzyme substrate;
KM apoptosis; protease; peptidase; apoptosis cascade; cancer;
KM chemotherapeutic agent; cell death; viral protease activity.

XX Synthetic.

OS WO9918856-A1.

PN 22-APR-1999.

PD 09-OCT-1998; 98WO-US21231.

PF 03-MAR-1998; 98US-0031661.

PR 10-OCT-1997; 97US-0061582.

XX (CYTO-) CYTOVIA INC.

XX Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;

XX PI

DR WPI; 1999-312448/26.
 XX
 PT New fluorogenic or fluorescent reporter molecules
 XX
 PS Claim 6; Page 165; 202pp; English.
 CC AAY15618-Y15759 represent peptides used to make the fluorogenic or
 CC fluorescent reporter molecules of the invention. These molecules
 CC contain a peptide moiety (e.g. present sequence) which acts as a
 CC substrate for enzymes involved in apoptosis or protease or peptidase
 CC enzymes. The compounds can be used as fluorogenic or fluorescent
 CC substrates for enzymes. Depending on the peptide moiety used, the
 CC fluorescent molecules can be used for detecting or measuring the
 CC activity of an enzyme involved in the apoptosis cascade in cells; to
 CC determine whether a test compound has an effect on an enzyme involved
 CC in the apoptosis cascade in cells; for determining the sensitivity of
 CC in a animal with cancer to treatment with chemotherapeutic agents or
 CC determining whether a test substance inhibits, prevents, causes or
 CC enhances cell death of test cells; for detecting or measuring the
 CC activity of a viral protease in cells; for determining whether a test
 CC compound has an effect on the activity of a viral protease in cells;
 CC and for measuring the activity or determining whether a test substance
 CC has an effect on the activity of a protease or peptidase in cells.
 CC
 SQ Sequence 4 AA;
 XX
 Query Match 70.0%; Score 14; DB 20; Length 4;
 Best Local Similarity 66.7%; Pred. No. 9.3e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LBP 4
 Db 1 IEP 3
 XX
 RESULT 6
 AAB28671
 ID AAB28671 standard; peptide; 4 AA.
 XX
 AC AAB28671;
 XX
 DT 13-FEB-2001 (first entry)
 XX
 DE Chemotactic peptide pepl.
 XX
 KW Chemotactic; osteopontin; vulnary; antiarthritic; antipsoriatic;
 KW cytostatic; antitumor; antiinflammatory; osteopachic;
 KW wound healing; cell migration; chemotaxis; atherosclerosis; cancer;
 KW angiogenic-associated disease; arthritis; psoriasis; haemangioma;
 KW ocular neovascularisation; cell apoptosis; nitrous oxide production;
 KW inflammation; osteoporosis; immune disease.
 XX
 OS Mammalia.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note="N-terminal acetyl"
 FT
 XX
 PN WO200063247-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 17-APR-2000; 2000WO-US10344.
 XX
 PR 15-APR-1999; 99US-0129764.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Ashkar S;
 XX
 PT WPI; 2000-687159/67.
 XX

PT New osteopontin-derived chemotactic and inhibitory peptides, useful for
 PT promoting scarless wound healing, modulating cellular chemotaxis,
 PT treating formation of atherosclerotic plaques and preventing metastasis
 PT
 XX
 PS Claim 17; Page 43; 54pp; English.
 CC The present sequence is an osteopontin-derived chemotactic peptide.
 CC Such chemotactic peptides are useful for promoting scarless wound
 CC healing, modulating chemotaxis and promoting cell migration to a target
 CC site in a cell of a subject. They are also used for modulating cellular
 CC chemotaxis in a mammalian cell such as smooth muscle cell, a macrophage,
 CC an endothelial cell, a vascular cell and a tumorigenic cell. They are
 CC useful for treating the formation of atherosclerotic plaques in a
 CC subject. The peptides are used for preventing metastasis, treating an
 CC angiogenic-associated disease such as arthritis, psoriasis, haemangioma,
 CC tumour metastasis or ocular neovascularisation. They are also used for
 CC activating cell apoptosis, for modulating nitrous oxide production and
 CC for inducing chemotaxis. The peptides are useful for diagnosing, treating
 CC and preventing tumour metastasis, inflammation, osteoporosis and immune
 CC diseases. They can also be used to enhance an immune response by
 CC attracting macrophages.
 CC
 SQ Sequence 4 AA;
 XX
 Query Match 70.0%; Score 14; DB 21; Length 4;
 Best Local Similarity 50.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLBP 4
 Db 1 MLDP 4
 XX
 RESULT 7
 AAB22909
 ID AAB22909 standard; peptide; 4 AA.
 XX
 AC AAB22909;
 XX
 DT 10-JUN-2001 (first entry)
 XX
 DE Granzyme B substrate recognition sequence, SEQ ID NO:100.
 XX
 KW Bioreceptor protein; fusion protein; recognition site;
 KW cellular targeting sequence; cellular localisation; fluorescent protein;
 KW protease activity detection; toxin detection; cellular stress detection;
 KW drug discovery; cell based screening; protease recognition site;
 KW cleavage site.
 XX
 OS Unidentified.
 OS
 XX
 PN WO200050872-A2.
 XX
 PD 31-AUG-2000.
 XX
 PF 25-FEB-2000; 2000WO-US04794.
 XX
 PR 26-FEB-1999; 99US-0122152.
 PR 08-MAR-1999; 99US-0123199.
 PR 12-JUL-1999; 99US-0352171.
 XX
 PA (CELL-) CELLOWICS INC.
 XX
 PI Giuliano KA, Kapur R,
 XX
 DR WPI; 2000-594086/56.
 DR N-PSDB; AAA93400.
 XX
 PT Automated cell-based characterization of toxin by contacting cells
 PT containing luminescent reporter molecules with test substance and
 PT analyzing optically
 XX

PS Example 11; Fig 29B; 336pp; English.

XX The invention relates to systems, methods and reagents for cell-based
CC screening or detection of compounds which affect particular biological
CC functions. The methods of the invention utilise fluorescent bioreactor
CC molecules which, when acted on by a compound of interest, cause an
CC alteration in the cellular distribution of at least the fluorescent
CC moiety. In one embodiment, the biosensors comprise heat shock proteins
CC (HSPs) fused to a fluorescent protein (e.g., jellyfish green fluorescent
CC protein (GFP), or derivatives thereof). Such biosensors are located in
CC the cytoplasm, but on stress activation translocate to the nucleus. In
CC another embodiment bioreactor proteins can be used to detect protease
CC activity. Such protease bioreactor fusion proteins comprise one or more
CC fluorescent proteins; a recognition signal which is cleaved by the
CC protease; and at least one cellular localisation signal. The latter two
CC components may be components of a single protein which is acted upon by
CC the protease, or may be from heterologous sources. Due to the
CC localisation signal, the bioreactor protein is localised to a
CC particular region of the cell. Once acted on by the protease of interest,
CC the fluorescent protein is cleaved from the localisation sequence, and
CC is free to migrate to other locations within the cell. The presence of a
CC second localisation signal attached to the fluorescent protein enables
CC the fluorescent protein to be directed to a different cellular
CC compartment after cleavage of the protease recognition sequence. The
CC change in distribution of the fluorescent protein can be detected using
CC imaging methods with a high degree of spatial resolution. The methods
CC and biosensors of the invention can be used to investigate a wide range
CC of cellular activities and to screen compounds which modulate these
CC activities. Biosensors containing a recognition site for caspase, for
CC example, may be used for the screening of compounds which modulate
CC apoptosis, while biosensors containing other protease recognition sites
CC may be used for the detection of proteolytic toxins (such as anthrax
CC lethal factor). The method provides improved target validation and
CC candidate compound optimisation by combining many cell screening formats
CC with fluorescence-based molecular reagents and computer-based feature
CC extraction, data analysis and automation, resulting in increased
CC quantity and speed of data collection and faster evaluation of drug
CC candidates. Sequences AAB22886-822920 and AAB22935 represent protease
CC recognition sites which may be used as components of biosensor fusion
CC proteins of the invention.

XX Sequence 4 AA;

Query Match 70.0%; Score 14; DB 21; Length 4;

Best Local Similarity 66.7%; Pred. No. 9.3e+05; Indels 0; Gaps 0;

QY 2 LBP 4

DB 1 IEP 3

RESULT 8

AA79611 ID AAY79611 standard; Peptide; 4 AA.

XX AAY79611;

AC AAY79611;

DT 29-AUG-2000 (first entry)

XX Granzyme-B substrate recognition sequence.

DE Granzyme-B substrate recognition sequence.

XX Protease; biosensor; granzyme-B; substrate recognition sequence;

XX cell screening; assay; analysis; drug discovery.

XX Unidentified.

XX MO200026408-A2.

XX 11-MAY-2000.

XX 29-OCT-1999; 99WO-US25431.

PR 30-OCT-1998; 98US-0106308.

PR 26-MAY-1999; 99US-0136078.

XX (CELL-) CELLOMICS INC.

PI Guiliano KA, Bright G, Olson K, Burroughs-Tencza S;

DR MPI; 2000-365644/31.

DR N-PSDB; AAA27600.

PT Recombinant nucleic acid encoding a protease biosensor useful for

PT fluorescence based cell and molecular biochemical assays for drug

PT discovery comprising three operably linked nucleic acid sequences

XX Claim 15; Fig 29B; 218pp; English.

CC The present sequence is that of a granzyme-B substrate
CC recognition sequence, which can be included in novel recombinant
CC protease biosensors (PBs) of the invention. The PBs (see AAY79638-54)
CC comprise: a first domain (see AAY79579-87) comprising at least 1
CC detectable polypeptide signal; a second domain (see AAY79588-622)
CC comprising at least 1 protease recognition site, such as the
CC present sequence; and a third domain (see AAY79623-37) comprising at
CC least 1 reactant target sequence. A recombinant nucleic acid (see
CC AAA27627-43) encoding the PB, an expression vector, and a genetically
CC engineered host cell are also claimed. A claimed method for
CC identifying compounds that modify protease activity in a cell
CC involves contacting a host cell that possesses the recombinant PB
CC with a test compound, and determining the PB distribution in the
CC host cell, where changes in the distribution of the PB are
CC correlated with modification of protease activity by the test
CC compound. Claimed kits for identifying compounds that modify
CC protease activity in a host cell include the recombinant nucleic
CC acid, or the recombinant PB, or the vector, or the host cell. The
CC PB is useful in high content screens to detect in vivo activation
CC of enzymatic activity, and to identify specific activity based on
CC cleavage of a known recognition motif.

XX Sequence 4 AA;

Query Match 70.0%; Score 14; DB 21; Length 4;

Best Local Similarity 66.7%; Pred. No. 9.3e+05; Indels 0; Gaps 0;

QY 2 LBP 4

DB 1 IEP 3

RESULT 9

AA80804 ID AAY80804 standard; peptide; 4 AA.

XX AAY80804;

AC AAY80804;

DT 22-MAY-2000 (first entry)

XX Fluorophore-labelled granzyme B substrate peptide, SEQ ID NO.23.

DE Protease substrate; fluorescent label; fluorophore; rhodamine;

XX blocking group; halobenzoyle group; cleavage; caspase; viral protease;

XX methionine aminopeptidase type 2; MetAP-2; drug screening.

XX Synthetic.

XX MO200004914-A1.

XX 03-FEB-2000.

XX 21-JUL-1999; 99WO-US16423.

XX 21-JUL-1998; 98US-0093642.

PA (CYTO-) CYTOVIA INC.
 PA (ZHAN/) ZHANG H.
 PA (CAIS/) CAI S X.
 PA (DREW/) DREWE J A.
 PA (YANG/) YANG W.
 XX Zhang H, Cai SX, Drewe JA, Yang W,
 DR WPI; 2000-195079/17.
 XX
 PT New fluorescently labeled amino acids or peptides, used as substrates
 PT for detecting enzymes or their modulators, e.g. anticancer or antiviral
 PT agents, contains a halobenzoyl N-blocking group
 XX
 PS Claim 3; Page 100; 174pp; English.
 XX
 CC The invention relates to fluorescently labelled peptides containing
 CC a halobenzoyl group on the fluorophore. They are of the structure
 CC peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking
 CC group, Y is a fluorescent or fluorogenic moiety (preferably a
 CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being
 CC assayed. The labelled peptides are reporters for detecting intracellular
 CC proteolytic enzymes, particularly caspases and other enzymes involved in
 CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human
 CC cytomegalovirus and hepatitis C virus proteases); and methionine
 CC aminopeptidase type 2 (MetAP-2). The peptides are particularly used to
 CC identify modulators of these enzymes which may be potentially useful as
 CC agents for treating conditions such as cancer, neurodegeneration,
 CC autoimmune diseases, myocardial infarction and viral infection.
 CC Modulators identified may also be used to prolong the life of cells being
 CC cultured for recombinant protein production, or to monitor the treatment
 CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are
 CC potential anti- angiogenic or anticancer agents. Sequences
 CC AA80782-Y80910 represent peptides, some of which are specifically
 CC claimed, which may be used in assay methods according to the invention.
 XX
 SQ Sequence 4 AA;
 QY
 Db Query Match 70.0%; Score 14; DB 21; Length 4;
 Best Local Similarity 66.7%; Pred. No. 9.3e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LEP 4
 :||
 1 IEP 3
 Db
 RESULT 10
 AAU79766
 ID AAU79766 standard; peptide; 4 AA.
 XX
 AC AAU79766;
 XX
 DT 30-JUN-2002 (first entry)
 XX
 DE Chicken bone derived peptide #1, useful as ACE inhibitor.
 XX
 KM Angiotensin converting enzyme inhibitor; ACEI; health food;
 KM food additive; pharmaceutical product; lowering blood pressure;
 KM hypertension; chicken essence by-product; chicken bone.
 XX
 OS Gallus sp.
 XX
 PN JP2001163896-A.
 XX
 PD 19-JUN-2001.
 XX
 PF 03-APR-2000; 2000JP-0105410.
 XX
 PR 01-DEC-1999; 99TW-0120997.
 XX
 PA (FOOD-) FOOD IND RES & DEV INST.
 XX

DR WPI; 2001-574451/65.
 XX
 PT New peptides capable of inhibiting angiotensin converting enzyme for
 PT use in pharmaceutical compositions, in health foods and as food
 PT additives
 XX
 PS Claim 1; Page 2; 39pp; Japanese.
 XX
 CC The present invention relates to novel peptides having angiotensin
 CC converting enzyme (ACE) inhibitory activity. Also described are
 CC methods for preparing products having ACE inhibitory activity, a
 CC pharmaceutical composition for use in the inhibition of ACE, and
 CC a health food or a food additive for use in the inhibition of
 CC ACE. The peptides of the invention are useful as ACE inhibitors (ACEI).
 CC They are useful in pharmaceutical products and health foods, and as
 CC food additives. Such compositions may be used for lowering blood pressure
 CC and treating hypertension. The manufacturing cost of the peptides of the
 CC invention is considerably less than prior art as the peptide can be
 CC produced from waste materials. Also the values of chicken essence
 CC by-products can be improved. The present peptide derived from chicken
 CC bone is useful as an ACE inhibitor.
 XX
 SQ Sequence 4 AA;
 QY
 Db Query Match 70.0%; Score 14; DB 22; Length 4;
 Best Local Similarity 75.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VLEP 4
 :||
 1 VLPP 4
 Db
 RESULT 11
 AAB82937
 ID AAB82937 standard; Peptide; 4 AA.
 XX
 AC AAB82937;
 XX
 DT 21-DEC-2001 (first entry)
 XX
 DE Granzyme B peptide substrate.
 XX
 KM Granzyme B; caspase; prodrug; therapy; ADEPT; cancer; tumour;
 KM inflammation; infection.
 XX
 OS Synthetic.
 XX
 PN WO200162300-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 22-FEB-2001; 2001WO-US05709.
 XX
 PR 24-FEB-2000; 2000US-184779P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Carter PJ, Gazzard L;
 XX
 DR WPI; 2001-611217/70.
 XX
 PT Delivering active agents to cell-types of interest for therapeutic
 PT purposes, comprises administering a cell-type targeted caspase
 PT conjugate and a pro-agent which is converted to the active agent in the
 PT presence of the caspase
 XX
 PS Disclosure; Page 13; 61pp; English.
 XX
 CC The present sequence is that of the preferred peptide substrate
 CC of granzyme-B. The invention provides methods for the localised
 CC delivery of pharmaceutical agents by the administration of a
 CC caspase conjugate that targets a cell type of interest and the

CC additional administration of a pro-agent, which is locally
CC converted by the caspase to an active agent. In preferred
CC embodiments the targeting component is an antibody, the drug is
CC preferably a cytotoxic or chemotherapeutic agent, and the
CC product moiety comprises a caspase-cleavable peptide, especially
CC a group II caspase cleavable peptide (see AAB82926), which is a
CC very poor substrate for granzyme B and for proinflammatory
CC caspases. The methods allow treatment of diseases or disorders
CC characterised by the appearance or presence of a particular cell
CC type. Such cells include bacterially and virally infected cells
CC expressing cell surface epitopes characteristic of the infection,
CC neoplastic and malignant cells such as tumour cells, and cells
CC characterised by their presence or appearance in areas of
CC inflammation.
CC
XX

Sequence 4 AA;

Query Match 70.0%; Score 14; DB 22; Length 4;
Best Local Similarity 66.7%; Pred. No. 9.3e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
: ||
Db 1 IEP 3

RESULT 12

AAG62561
ID AAG62561 standard; peptide; 4 AA.

AC AAG62561;

DT 05-SEP-2001 (first entry)

DE Cresyl violet substituted caspase inhibitor substrate SEQ ID NO: 16.

XX Caspase inhibitor substrate; cresyl violet; fluorogenic substrate;

KW metastasis; cancer; protease.

XX Synthetic.

OS Key Location/Qualifiers

FT Modified-site 1 /label= OTHER
FT /note="optionally modified by carbobenzoxy or acetyl"

XX US6235493-B1.

XX 22-MAY-2001.

XX 05-AUG-1998; 98US-0130193.

XX 06-AUG-1997; 97US-0055392.

XX (REGC) UNIV CALIFORNIA.

XX Bissell ER, Smith RF;

XX WPI; 2001-431695/46.

XX Method for detection of an enzyme in vivo or in vitro in a cell using
XX an amino acid-substituted cresyl violet fluorogenic substrate -

XX Claim 6; Column 32; 27pp; English.

XX The present invention describes a method of detecting the presence of an
XX enzyme in living cells, involving contacting the cell with an amino acid
XX substituted cresyl violet fluorogenic substrate and quantifying the
XX fluorescence produced. This is particularly useful for detecting enzymes
XX such as proteases and caspases, which may be linked to cancer metastasis.
XX The present sequence is a caspase inhibitor substrate used in the
XX exemplification of the invention.

Sequence 4 AA;

Query Match 70.0%; Score 14; DB 22; Length 4;
Best Local Similarity 66.7%; Pred. No. 9.3e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
: ||
Db 1 IEP 3

RESULT 13

AAB29759

ID AAB29759 standard; peptide; 4 AA.

AC AAB29759;

DT 28-FEB-2001 (first entry)

DE Escherichia coli ribosomal protein L16 N-terminus.

XX Recombinant human haemoglobin; rhb1.1; bacterial expression;

KW N-terminal methionine methylation signal; demethylation;

KW Escherichia coli; non-immunogenic; pharmaceutical composition.

XX Escherichia coli.

OS US6140071-A.

XX 31-OCT-2000.

XX 27-JAN-1994; 94US-0188374.

XX 27-JAN-1994; 94US-0188374.

XX (SOMA-) SOMATOGEN INC.

XX Altken JF, Apostol IZ, Levine JD, Lippincott JA;

XX WPI; 2001-048957/06.

XX Decreasing methylation of an N-terminus protein, especially hemoglobin
XX having proline at amino acid position 4, useful for producing
XX demethylated proteins for treating diseases, by altering this amino
XX acid to a non-proline residue -

XX Disclosure; Column 1; 26pp; English.

XX The invention relates to a method of decreasing the amount of N-terminal
XX methionine methylation on a protein expressed in a bacterium. The
XX bacterial methyltransferase which directs N-terminal methionine
XX methylation recognises proteins which have a proline residue at position
XX 4 (e.g., the bacterial ribosomal protein L16 and the bacterial chemotaxis
XX protein CheZ). The method comprises introducing mutations into the DNA
XX encoding the protein so that residue 4 is a non-proline residue, thereby
XX reducing the degree of N-terminal methylation when the protein is
XX expressed in a bacterium. The method is useful for decreasing methylation
XX of a protein, particularly a recombinantly produced protein. The
XX demethylated protein can be used in a pharmaceutical composition for
XX the treatment of a disease but with less likelihood of eliciting an
XX immunological response. These demethylated proteins may be used as
XX therapeutic agent for the treatment and/or amelioration of disease or
XX symptoms associated with a disease. The exemplifications describe
XX the expression of a recombinant human haemoglobin construct (rhb1.1) in
XX Escherichia coli, and its modification such that residue 4 of the
XX di-alpha chain of the recombinant haemoglobin is altered from proline
XX to a non-proline residue. The present sequence represents a peptide
XX referred to in the disclosure of the invention.

Sequence 4 AA;

Query Match 70.0%; Score 14; DB 22; Length 4;
Best Local Similarity 50.0%; Pred. No. 9.3e+05;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
:|:|
Db 1 MLQP 4

RESULT 14

AAE28993
ID AAE28993 standard; peptide: 4 AA.

XX AAE28993;

DT 27-JAN-2003 (first entry)

XX Human thrombin cleavage site.

XX Vector; prokaryotic cell; human; thrombin cleavage site.

XX Homo sapiens.

PN WO200272847-A2.

PD 19-SEP-2002.

PF 22-FEB-2002; 2002WO-US05069.

PR 09-MAR-2001; 2001US-274384P.

XX (GETH) GENENTECH INC.

PI Paegle ES, Reilly D, Yansura DG;

XX WPI; 2002-723363/78.

XX New vector comprising anti-termination nucleic acid or RNA encoding the

PT polypeptide with a non-lambda promoter, useful for producing human

PT thrombopietin (TPO) or fibroblast growth factor-5 (FGF-5) polypeptide

XX Example 1; Page 21; 70pp; English.

XX The invention relates to vectors for producing a polypeptide heterologous

CC to prokaryotic cells and method for producing the polypeptide. The method

CC is useful for producing a polypeptide heterologous to prokaryotic cells.

CC The present sequence is human thrombin cleavage site used in the

CC exemplification of the invention.

XX Sequence 4 AA;

XX Query Match 70.0%; Score 14; DB 23; Length 4;

XX Best Local Similarity 66.7%; Pred. No. 9.3e+05; Indels 0; Gaps 0;

XX Matches 2; Conservative 1; Mismatches 0;

XX Db 2 LEP 4

XX 1 IEP 3

XX 27-NOV-2002 (first entry)

XX Protease biosensor recognition site #24.

XX Detection; classification; identification; toxin detection;

XX protease; ADP-ribosylating toxin; cytotoxic phospholipase;

XX exfoliative toxin; toxic threat agent.

OS Synthetic.

XX US6416959-B1.

XX 09-JUL-2002.

XX 25-FEB-2000; 2000US-0513783.

XX 26-FEB-1999; 99US-122152P.

XX 08-MAR-1999; 99US-123399P.

XX 31-AUG-1999; 99US-151787P.

XX 01-DEC-1999; 99US-168408P.

XX 27-FEB-1997; 97US-0810983.

XX 27-FEB-1998; 98US-0031271.

XX 12-JUL-1999; 99US-0352171.

XX 17-SEP-1999; 99US-0398965.

XX 29-OCT-1999; 99US-0430656.

XX (GIUL/) GIULIANO K.

XX (KAPU/) KAPUR R.

XX Giuliano K, Kapur R;

XX WPI; 2002-634730/68.

XX N-PSDB; ABS71518.

XX Automated cell-based toxin detection, classification, and/or

PT identification by treating cells involves use of three classes of

PT luminescent reporter molecules such as detectors, classifiers or

PT identifiers -

XX Example 10; Fig 29B; 214pp; English.

XX The invention describes methods of automated detection, classification

CC and identification comprising treating cells containing luminescent

CC reporter molecules (1) in array of locations with a test substance, where

CC (1) are detectors, classifiers or identifiers, imaging cells in each

CC location to obtain luminescent signals and converting optical information

CC into digital data to interpret presence of toxins in the test substance.

CC The method are useful for detection of toxins chosen from proteases,

CC ADP-ribosylating toxins, cytotoxic phospholipases, and exfoliative

CC toxins. Three classes of cell-based luminescent reporter molecules

CC such as detectors, classifiers and identifiers are described and serve

CC as reporters of toxic threat agents. The first two levels of

CC characterisation ensure a rapid readout of toxin class without

CC sacrificing the ability to detect many new mutant toxins or dissect

CC several complex mixtures of known toxins. This is the amino acid sequence

CC of a protease biosensor recognition site used in the cell-based screening

XX system.

XX Sequence 4 AA;

XX Query Match 70.0%; Score 14; DB 23; Length 4;

XX Best Local Similarity 66.7%; Pred. No. 9.3e+05; Indels 0; Gaps 0;

XX Matches 2; Conservative 1; Mismatches 0;

XX Db 2 LEP 4

XX 1 IEP 3

XX Search completed: November 25, 2003, 14:06:39

XX Job time : 42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 14:07:53 ; Search time 29 Seconds
(without alignments)
25.440 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20

Sequence: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues

Total number of hits satisfying chosen parameters: 4771

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	4	US-09-729-873-16	Sequence 16, Appl
2	20	100.0	4	US-09-732-411-15	Sequence 15, Appl
3	20	100.0	4	US-10-091-724-7	Sequence 7, Appl
4	14	70.0	4	US-09-729-873-24	Sequence 24, Appl
5	14	70.0	4	US-09-947-387-23	Sequence 23, Appl
6	14	70.0	4	US-10-138-375-23	Sequence 23, Appl
7	14	70.0	4	US-10-100-957A-100	Sequence 100, App
8	14	70.0	4	US-10-080-866-6	Sequence 6, Appl
9	13	65.0	4	US-09-947-387-27	Sequence 27, Appl
10	13	65.0	4	US-09-932-165-1436	Sequence 1436, Ap
11	13	65.0	4	US-10-319-592-5	Sequence 5, Appl
12	13	65.0	4	US-10-138-375-27	Sequence 27, Appl
13	13	65.0	4	US-10-006-869-199	Sequence 199, App
14	12	60.0	3	US-09-834-240-32	Sequence 32, Appl
15	12	60.0	3	US-10-001-073-12	Sequence 12, Appl

16	12	60.0	4	US-09-947-387-13	Sequence 13, Appl
17	12	60.0	4	US-09-809-638-733	Sequence 733, App
18	12	60.0	4	US-09-852-910-169	Sequence 169, App
19	12	60.0	4	US-10-285-045-56	Sequence 56, Appl
20	12	60.0	4	US-10-076-047A-115	Sequence 115, App
21	12	60.0	4	US-10-284-660-56	Sequence 56, Appl
22	12	60.0	4	US-10-087-942-8	Sequence 8, Appl
23	12	60.0	4	US-10-196-394-120	Sequence 120, App
24	12	60.0	4	US-10-138-375-13	Sequence 13, Appl
25	12	60.0	4	US-10-087-905-8	Sequence 8, Appl
26	12	60.0	4	US-10-059-261-25	Sequence 25, Appl
27	12	60.0	4	US-10-053-261-133	Sequence 133, App
28	12	60.0	4	US-10-006-869-197	Sequence 197, App
29	12	60.0	4	US-10-205-270-4	Sequence 4, Appl
30	12	60.0	4	US-10-096-986-7	Sequence 7, Appl
31	12	60.0	4	US-10-096-986-31	Sequence 31, Appl
32	11	55.0	4	US-09-861-097-16	Sequence 16, Appl
33	11	55.0	4	US-09-861-098-16	Sequence 16, Appl
34	11	55.0	4	US-09-791-153A-42	Sequence 42, Appl
35	11	55.0	4	US-10-169-351-94	Sequence 94, Appl
36	11	55.0	4	US-10-022-066-163	Sequence 163, App
37	11	55.0	4	US-09-861-012-16	Sequence 16, Appl
38	11	55.0	4	US-10-277-292-677	Sequence 677, App
39	11	55.0	4	US-10-280-340-577	Sequence 677, App
40	11	55.0	4	US-10-006-869-269	Sequence 269, App
41	11	55.0	4	US-10-006-869-462	Sequence 462, App
42	11	55.0	4	US-10-006-869-476	Sequence 476, App
43	11	55.0	4	US-10-006-869-574	Sequence 574, App
44	11	55.0	4	US-10-012-466A-45	Sequence 45, Appl
45	10	50.0	3	US-09-031-629A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-729-873-16
; Sequence 16, Application US/09729873
; Patent No. US2001003692A1
GENERAL INFORMATION:
APPLICANT: Samy Ashkar
TITLE OF INVENTION: Osteopontin-Derived Chemotactic and Inhibitory Agents
FILE REFERENCE: CM2-123CP
CURRENT APPLICATION NUMBER: US/09/729, 873
CURRENT FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 60/129, 764
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: PCT/US00/10344
PRIOR FILING DATE: 2000-04-17
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-729-873-16
Query Match 100.0%; Score 20; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
QY 1 VLEP 4
1111
1 VLEP 4
Db 1 VLEP 4
RESULT 2
US-09-732-411-15
; Sequence 15, Application US/09732411

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; Patent No. US20020058336A1
; GENERAL INFORMATION:
; APPLICANT: Samy Ashkar
; TITLE OF INVENTION: Adhesion Modulatory Peptides and Methods for Use
; FILE REFERENCE: CM2-124CP
; CURRENT APPLICATION NUMBER: US/09/732,411
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/129,709
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: PCT/US00/10329
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
US-09-732-411-15
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Query Match          100.0%; Score 20; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 VLEP 4
        |||
Db       1 VLEP 4
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RESULT 3

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US-10-091-724-7
; Sequence 7, Application US/10091724
; Publication No. US20030105310A1
; GENERAL INFORMATION:
; APPLICANT: Children's Medical Center Corporation
; APPLICANT: Ashkar, Samy
; TITLE OF INVENTION: Method to Screen Peptide Libraries Using Minicell Display
; FILE REFERENCE: CMCC 820
; CURRENT APPLICATION NUMBER: US/10/091,724
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 60/306,946
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/274,039
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Inhibitor of macrophage recruitment.
US-10-091-724-7
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Query Match          100.0%; Score 20; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 VLEP 4
        |||
Db       1 VLEP 4
```

RESULT 4

```
US-09-729-873-24
; Sequence 24, Application US/09729873
; Patent No. US20010036921A1
; GENERAL INFORMATION:
; APPLICANT: Samy Ashkar
; TITLE OF INVENTION: Osteopontin-Derived Chemotactic and Inhibitory Agents
; TITLE OF INVENTION: and Uses Therefor
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; FILE REFERENCE: CM2-123CP
; CURRENT APPLICATION NUMBER: US/09/729,873
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/129,764
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/US00/10344
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
; OTHER INFORMATION: Peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: ACETYLYATION
US-09-729-873-24
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Query Match          70.0%; Score 14; DB 9; Length 4;
Best Local Similarity 50.0%; Pred. No. 6e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 VLEP 4
        |||
Db       1 MUDP 4
```

RESULT 5

```
US-09-947-387-23
; Sequence 23, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. US20020150885A1a1 Fluorogenic or Fluorescent Reporter Molecu
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-23
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Query Match          70.0%; Score 14; DB 10; Length 4;
Best Local Similarity 66.7%; Pred. No. 6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      2 LEP 4
        |||
Db       1 LEP 3
```

```
RESULT 6
US-10-138-375-23
; Sequence 23, Application US/10138375
; Publication No. US20030208037A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. US20030208037A1 Fluorescence Dyes and Their Applications for
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease
; FILE REFERENCE: 1735.0030001
; CURRENT FILING DATE: 2002-05-06
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-138-375-23

Query Match
Best Local Similarity 70.0%; Score 14; DB 12; Length 4;
Best Local Similarity 66.7%; Pred. No. 6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
: |||
Db 1 IEP 3

RESULT 7
US-10-100-957A-100
; Sequence 100, Application US/10100957A
; Publication No. US20030096322A1
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-L1A
; CURRENT FILING DATE: 2002-03-19
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 100
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Granzyme B
; OTHER INFORMATION: substrate recognition sequence
US-10-100-957A-100

Query Match
Best Local Similarity 70.0%; Score 14; DB 15; Length 4;
Best Local Similarity 66.7%; Pred. No. 6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
: |||
Db 1 IEP 3

RESULT 8
US-10-080-866-6
; Sequence 6, Application US/10080866
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; Publication No. US20030109024A1
; GENERAL INFORMATION:
; APPLICANT: Peggie, E. Sasha
; APPLICANT: Reilly, Dorothea
; APPLICANT: Yaneura, Daniel G.
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF POLYPEPTIDES
; FILE REFERENCE: P1732R1
; CURRENT FILING DATE: 2002-02-22
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-866-6

Query Match
Best Local Similarity 70.0%; Score 14; DB 15; Length 4;
Best Local Similarity 66.7%; Pred. No. 6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
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Db 1 IEP 3

RESULT 9
US-09-947-387-27
; Sequence 27, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. US20020150885A1 Fluorogenic or Fluorescent Reporter Molecul
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; FILE REFERENCE: 1735.0290005
; CURRENT FILING DATE: 2001-09-07
; PRIOR FILING DATE: 1997-10-10
; PRIOR FILING DATE: 1998-03-03
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-27

Query Match
Best Local Similarity 65.0%; Score 13; DB 10; Length 4;
Best Local Similarity 66.7%; Pred. No. 6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
: |||
Db 1 IEP 3

RESULT 10
US-09-932-165-1436
; Sequence 1436, Application US/09932165
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Publication No. US20030134784A1
GENERAL INFORMATION:
APPLICANT: RATTANO, ARTHUR
APPLICANT: CHALLITA-ETD, PIA M.
APPLICANT: FARIS, MARY
APPLICANT: SAFEHRAN, DOUGLAS
APPLICANT: AFEAR, DANIEL
APPLICANT: LEVIN, ELIANA
APPLICANT: HUBERT, RENE
APPLICANT: GE, WANGMAO
APPLICANT: JAKOBOVITS, AVA
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
TITLE OF INVENTION: 83P2H3 AND CatrP2E11 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20014.00
CURRENT APPLICATION NUMBER: US/09/932.165
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/226,329
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1436
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1436

Query Match 65.0%; Score 13; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
|||
DB 2 VLE 4

RESULT 11
US-10-319-592-5
Sequence 5, Application US/10319592.
Publication No. US20030152567A1
GENERAL INFORMATION:
APPLICANT: ROMISCH, JURGEN
APPLICANT: FEUBNER, ANNETTE
APPLICANT: STORR, HANS-ARNOLD
TITLE OF INVENTION: PROTEASE FOR ACTIVATING CLOTTING FACTOR VII
FILE REFERENCE: 06478.1424
CURRENT APPLICATION NUMBER: US/10/319.592
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: US/09/295.316
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 19818495.6
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 1982734.2
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 19851332.1
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 19851336.4
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 19851335.6
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 19903693.4
PRIOR FILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 4
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Illustrative
OTHER INFORMATION: peptide

US-10-319-592-5

Query Match 65.0%; Score 13; DB 12; Length 4;
Best Local Similarity 66.7%; Pred. No. 6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
|||
DB 2 LDP 4

RESULT 12
US-10-138-375-27
Sequence 27, Application US/10138375
Publication No. US20030208037A1
GENERAL INFORMATION:
APPLICANT: Zhang, Han-Zhong
APPLICANT: Cai, Sui Xiong
APPLICANT: Drewe, John A.
APPLICANT: Yang, Wu
TITLE OF INVENTION: No. US20030208037A1 Fluorescence Dyes and Their Applications f
TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteas
FILE REFERENCE: 1735.0030001
CURRENT APPLICATION NUMBER: US/10/138.375
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357.952
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093.642
PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
NUMBER OF SEQ ID NOS: 139
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-138-375-27

Query Match 65.0%; Score 13; DB 12; Length 4;
Best Local Similarity 66.7%; Pred. No. 6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
|||
DB 1 VEP 3

RESULT 13
US-10-006-869-199
Sequence 199, Application US/10006869
Publication No. US20030082166A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CAHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C7
CURRENT APPLICATION NUMBER: US/10/006.869
CURRENT FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 199
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative linear modulating agent based on
OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-10-006-869-199

Query Match 65.0%; Score 13; DB 15; Length 4;
 Best Local Similarity 66.7%; Pred. No. 6e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 EP 4
 : ||
 Db 1 VEP 3

RESULT 14

US-09-834-240-32
 ; Sequence 32, Application US/09834240
 ; Publication No. US20030166261A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sompuram, Seeshi R.
 ; APPLICANT: Ramanathan, Halaasya
 ; TITLE OF INVENTION: Quality Control for Cytochemical Assays
 ; FILE REFERENCE: 1159.1008-005
 ; CURRENT APPLICATION NUMBER: US/09/834,240
 ; CURRENT FILING DATE: 2003-03-28
 ; PRIOR APPLICATION NUMBER: 09/549,855
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 09/291,351
 ; PRIOR FILING DATE: 1999-04-14
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 32
 ; LENGTH: 3
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-834-240-32

Query Match 60.0%; Score 12; DB 12; Length 3;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 EP 4
 : ||
 Db 2 EP 3

RESULT 15

US-10-001-073-12
 ; Sequence 12, Application US/10001073
 ; Publication No. US20030113725A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liggett, Stephen
 ; APPLICANT: Small, Kirsten
 ; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
 ; FILE REFERENCE: 13073-PCT
 ; CURRENT APPLICATION NUMBER: US/10/001,073
 ; CURRENT FILING DATE: 2001-11-01
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 3
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-001-073-12

Query Match 60.0%; Score 12; DB 15; Length 3;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 EP 4
 : ||
 Db 2 EP 3

Search completed: November 25, 2003, 14:13:04
 Job time : 30 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 14:05:52 ; Search time 21 Seconds
(without alignments)
8.059 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20

Sequence: 1 VLEP 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 10151

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:

1: /cgn2_6/prodata/1/aa/5A COMB.pep.*
2: /cgn2_6/prodata/1/aa/5A COMB.pep.*
3: /cgn2_6/prodata/1/aa/5A COMB.pep.*
4: /cgn2_6/prodata/1/aa/5A COMB.pep.*
5: /cgn2_6/prodata/1/aa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/aa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	15	75.0	4	1	US-08-240-712-5	Sequence 5, Appl
2	15	75.0	4	1	US-08-443-890-5	Sequence 5, Appl
3	15	75.0	4	3	US-09-058-562-5	Sequence 5, Appl
4	15	75.0	4	5	PCT-US92-09752-5	Sequence 5, Appl
5	14	70.0	4	1	US-08-336-343A-38	Sequence 38, Appl
6	14	70.0	4	2	US-08-609-271-1	Sequence 1, Appl
7	14	70.0	4	3	US-08-188-374-1	Sequence 16, Appl
8	14	70.0	4	3	US-09-130-193-16	Sequence 23, Appl
9	14	70.0	4	3	US-09-337-952-23	Sequence 23, Appl
10	14	70.0	4	4	US-09-521-650-23	Sequence 23, Appl
11	14	70.0	4	4	US-09-168-888-23	Sequence 23, Appl
12	14	70.0	4	4	US-09-513-783A-100	Sequence 100, Appl
13	14	70.0	4	2	US-08-441-871-28	Sequence 28, Appl
14	13	65.0	4	3	US-09-330-970-16	Sequence 16, Appl
15	13	65.0	4	3	US-09-330-970-34	Sequence 34, Appl
16	13	65.0	4	3	US-08-859-242-31	Sequence 31, Appl
17	13	65.0	4	3	US-09-357-552-27	Sequence 27, Appl
18	13	65.0	4	4	US-09-521-650-27	Sequence 27, Appl
19	13	65.0	4	4	US-09-168-888-27	Sequence 27, Appl
20	13	65.0	4	4	US-09-187-859-199	Sequence 199, Appl
21	13	65.0	4	4	US-09-295-316-5	Sequence 5, Appl
22	13	65.0	4	4	US-09-446-787B-45	Sequence 45, Appl
23	13	65.0	4	4	US-09-839-542B-199	Sequence 199, Appl
24	12	60.0	4	1	US-07-714-167E-8	Sequence 8, Appl
25	12	60.0	4	1	US-07-714-167E-11	Sequence 11, Appl
26	12	60.0	4	1	US-07-729-353-7	Sequence 7, Appl
27	12	60.0	4	1	US-08-122-546-1	Sequence 1, Appl

28	12	60.0	4	1	US-08-280-443-39	Sequence 39, Appl
29	12	60.0	4	1	US-08-457-459-39	Sequence 39, Appl
30	12	60.0	4	1	US-08-224-868-5	Sequence 5, Appl
31	12	60.0	4	1	US-08-555-678-39	Sequence 39, Appl
32	12	60.0	4	1	US-08-477-509B-7	Sequence 7, Appl
33	12	60.0	4	1	US-08-477-509B-31	Sequence 31, Appl
34	12	60.0	4	2	US-08-609-271-2	Sequence 2, Appl
35	12	60.0	4	2	US-08-609-271-3	Sequence 3, Appl
36	12	60.0	4	2	US-08-609-271-5	Sequence 5, Appl
37	12	60.0	4	2	US-08-764-938-1	Sequence 1, Appl
38	12	60.0	4	2	US-08-482-085B-7	Sequence 7, Appl
39	12	60.0	4	3	US-08-482-085B-31	Sequence 31, Appl
40	12	60.0	4	3	US-08-415-655-3	Sequence 3, Appl
41	12	60.0	4	3	US-08-624-405-7	Sequence 7, Appl
42	12	60.0	4	3	US-09-105-678A-50	Sequence 50, Appl
43	12	60.0	4	3	US-09-131-052-1	Sequence 1, Appl
44	12	60.0	4	3	US-08-188-374-2	Sequence 2, Appl
45	12	60.0	4	3	US-08-188-374-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-240-712-5
; Sequence 5, Application US/08240712
; Patent No. 5599907
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DAVID C.
; APPLICANT: MATHEWS, ANTONY JAMES
; APPLICANT: SETTLER, GARY L.
; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
; NUMBER OF INVENTIONS: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: Broadway and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,712
; FILING DATE: 09-MAY-1994
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09752
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P
; REGISTRATION NUMBER: 28,005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-240-712-5
Query Match 75.0%; Score 15; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLEP 4
Db 1 VLSP 4

RESULT 2

US-08-443-890-5
; Sequence 5, Application US/08443890
; Patent No. 5739011
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DAVID C.
; APPLICANT: MATHEWS, ANTONY JAMES
; APPLICANT: STETLER, GARY L.
; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; City: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,890
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/240,712
; FILING DATE: 09-MAY-1994
; APPLICATION NUMBER: PCT/US92/09752
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: ANDERSON=6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-443-890-5

Query Match 75.0%; Score 15; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLEP 4
Db 1 VLSP 4

RESULT 3

US-09-058-562-5
; Sequence 5, Application US/09058562A
; Patent No. 6184356
; GENERAL INFORMATION:
; APPLICANT: Anderson, David C.
; APPLICANT: Mathews, Antony James
; APPLICANT: Stetler, Gary L.
; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC HEMOGLOBINS

FILE REFERENCE: BXTB 2087
; CURRENT APPLICATION NUMBER: US/09/058,562A
; CURRENT FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 08/240,712
; PRIOR FILING DATE: 1994-05-09
; PRIOR APPLICATION NUMBER: PCT/US92/09752
; PRIOR FILING DATE: 1993-05-13
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-058-562-5

Query Match 75.0%; Score 15; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLEP 4
Db 1 VLSP 4

RESULT 4

PCT-US92-09752-5
; Sequence 5, Application PC/TUS9209752
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DAVID C.
; APPLICANT: MATHEWS, ANTONY JAMES
; APPLICANT: STETLER, GARY L.
; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; City: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09752
; FILING DATE: 19930109
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: ANDERSON-6-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US92-09752-5

Query Match 75.0%; Score 15; DB 5; Length 4;
Best Local Similarity 75.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 1 VLEP 4

RESULT 5

US-08-336-343A-38
; Sequence 38, Application US/08336343A
; Patent No. 5677144
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Axel
; TITLE OF INVENTION: CCK-2, A No. 5677144e1 Receptor Tyrosine Kinase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,343A
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-336-343A-38

Query Match 70.0%; Score 14; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
DB 2 MEP 4

RESULT 6

US-08-609-271-1
; Sequence 1, Application US/08609271
; Patent No. 5811264
; GENERAL INFORMATION:
; APPLICANT: Aitken, Jacqueline F.
; APPLICANT: Apostol, Izidor Z.
; APPLICANT: Lippincott, Julie A.
; APPLICANT: Levine, Joseph D.
; TITLE OF INVENTION: Proteins with Mutations to Decrease N-Terminal Methylation
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 2545 Central Avenue, Site FD-1
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.0a

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,271
FILING DATE: 28 February 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/188,374
FILING DATE: 1/27/94

ATTORNEY/AGENT INFORMATION:

NAME: No. 5811264e11, Marianne F.

REGISTRATION NUMBER: 38571

NAME: Brown, Theresa A.

REGISTRATION NUMBER: 32547

REFERENCE/DOCKET NUMBER: 170/Div

TELECOMMUNICATION INFORMATION:

TELEPHONE: 303-444-3013

TELEFAX: 303-444-3013

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: no

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /label=Modified-site1

OTHER INFORMATION: /note="Met(1) is Methylated N terminal Met"

US-08-609-271-1

Query Match 70.0%; Score 14; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.5e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 1 MLEP 4

RESULT 7

US-08-188-374-1
; Sequence 1, Application US/08188374B
; Patent No. 6140071
; GENERAL INFORMATION:
; APPLICANT: Aitken F., Jacqueline
; APPLICANT: Apostol, Izidor Z.
; APPLICANT: Lippincott, Julie A.
; APPLICANT: Levine, Joseph D.
; TITLE OF INVENTION: Proteins with Mutations to Decrease N-Terminal Meth
; FILE REFERENCE: BXTB 1953
; CURRENT APPLICATION NUMBER: US/08/188,374B
; CURRENT FILING DATE: 1994-01-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: METHYLATION- N terminal Met
US-08-188-374-1

Query Match 70.0%; Score 14; DB 3; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.5e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
: ||
Db 1 MLQP 4

RESULT 8

US-09-130-193-16
; Sequence 16, Application US/09130193
; Patent No. 6235493

GENERAL INFORMATION:

APPLICANT: EUGENE R. BISSELL ET AL
TITLE OF INVENTION: AMINO ACID SUBSTITUTED-
CRESTYL VIOLET, SYNTHETIC
TITLE OF INVENTION: FLUORESCENT SUBSTRATES
FOR THE ANALYSIS OF
TITLE OF INVENTION: AGENTS IN INDIVIDUAL IN
VIVO CELLS OR TISSUE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIK A, LLP
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
STATE: California
COUNTRY: United States of America
ZIP: 94306-1840

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage

COMPUTER:

OPERATING SYSTEM: DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,193

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/026,062

FILING DATE: SEPTEMBER 13, 1996

ATTORNEY/AGENT INFORMATION:

NAME: HOWARD W. PETERS

REGISTRATION NUMBER: 29,202

REFERENCE/DOCKET NUMBER: 3586-01-1(HMP)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 324-1677 X 20

TELEFAX: (650) 324-1678

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-130-193-16

Query Match 70.0%; Score 14; DB 3; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
: ||
Db 1 IEP 3

RESULT 9

US-09-357-952-23

; Sequence 23, Application US/09357952

; Patent No. 6248904

GENERAL INFORMATION:

APPLICANT: Zhang, Han-Zhong

APPLICANT: Cai, Sui Xiong

APPLICANT: Drewe, John A.

APPLICANT: Yang, Wu

TITLE OF INVENTION: No. 6248904e1 Fluorescence Dyes and Their Applications for Whole-
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteases

TITLE OF INVENTION: Other Enzymes and the Use Thereof

FILE REFERENCE: 1735.0030001

CURRENT APPLICATION NUMBER: US/09/357,952

CURRENT FILING DATE: 1999-07-21

EARLIER APPLICATION NUMBER: US 60/093,642

EARLIER FILING DATE: 21-JUL-1998

NUMBER OF SEQ ID NOS: 139

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 23

LENGTH: 4

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptide

US-09-357-952-23

Query Match 70.0%; Score 14; DB 3; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
: ||
Db 1 IEP 3

RESULT 10

US-09-521-650-23

; Sequence 23, Application US/09521650

; Patent No. 6335429

GENERAL INFORMATION:

APPLICANT: Weber, Eckard

APPLICANT: Cai, Sui Xiong

APPLICANT: Keana, John F.W.

APPLICANT: Drewe, John A.

TITLE OF INVENTION: No. 6335429e1 Fluorogenic or Fluorescent Reporter Molecules and

TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence

TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the

TITLE OF INVENTION: Use Thereof

FILE REFERENCE: 1735.0290002

CURRENT APPLICATION NUMBER: US/09/521,650

CURRENT FILING DATE: 2000-03-08

EARLIER APPLICATION NUMBER: 09/168,888

EARLIER FILING DATE: 1998-10-09

EARLIER APPLICATION NUMBER: US 60/061,582

EARLIER FILING DATE: 1997-10-10

EARLIER APPLICATION NUMBER: US 09/033,661

EARLIER FILING DATE: 1998-03-03

NUMBER OF SEQ ID NOS: 142

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 23

LENGTH: 4

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptide

US-09-521-650-23

Query Match 70.0%; Score 14; DB 4; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
: ||
Db 1 IEP 3

RESULT 11

US-09-168-888-23

; Sequence 23, Application US/09168888

; Patent No. 6342611

GENERAL INFORMATION:
APPLICANT: Weber, Eckard
APPLICANT: Cai, Sui Xiong
APPLICANT: Keana, John F.W.
APPLICANT: Drewe, John A.
APPLICANT: Zhang, Han-Zhong
TITLE OF INVENTION: No. 634261e1 Fluorogenic or Fluorescent Reporter Molecules and
TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
FILE REFERENCE: 1735-0290002
CURRENT APPLICATION NUMBER: US/09/166,888
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 60/061,582
EARLIER FILING DATE: 1997-10-10
EARLIER APPLICATION NUMBER: US 09/033,661
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 142
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-168-888-23

Query Match 70.0%; Score 14; DB 4; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
Db 1 IEP 3

RESULT 12
US-09-513-783A-100
Sequence 100, Application US/09513783A
Patent No. 6416959
GENERAL INFORMATION:
APPLICANT: Giuliano, Kenneth A.
APPLICANT: Kapur, Ravi
TITLE OF INVENTION: A System for Cell Based Screening
FILE REFERENCE: 97-022-11
CURRENT APPLICATION NUMBER: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 100
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Granzyme B
US-09-513-783A-100

Query Match 70.0%; Score 14; DB 4; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
Db 1 IEP 3

RESULT 13
US-08-441-871-28
Sequence 28, Application US/08441871
Patent No. 5846765
GENERAL INFORMATION:

APPLICANT: Matthews, David J.
APPLICANT: Wells, James A.
APPLICANT: Zoller, Mark J.
TITLE OF INVENTION: Identification of No. 5846765e1 Substrates
NUMBER OF SEQUENCES: 152
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,871
FILING DATE: 16-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/418928
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/161692
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/864452
FILING DATE: 06-APR-1992
APPLICATION NUMBER: PCT/US91/09133
FILING DATE: 03-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743614
FILING DATE: 09-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715300
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/683400
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/621667
FILING DATE: 03-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Daryl B.
REGISTRATION NUMBER: 32,637
REFERENCE/DOCKET NUMBER: 645P5C2D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1249
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-441-871-28

Query Match 65.0%; Score 13; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.5e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
Db 2 LDP 4

RESULT 14
US-09-330-970-16
Sequence 16, Application US/09330970
Patent No. 6146876

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; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: White, David
; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide
; TITLE OF INVENTION: Phosphodiesterase
; FILE REFERENCE: 5800-28
; CURRENT APPLICATION NUMBER: US/09/330,970
; CURRENT FILING DATE: 1999-06-11/277,423
; EARLIER APPLICATION NUMBER: 09/277,423
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-330-970-16

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Query Match          65.0%; Score 13; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VLE 3
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Db      2 VLE 4

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RESULT 15
US-09-330-970-34
; Sequence 34, Application US/09330970
; Patent No. 6146876
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: White, David
; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide
; TITLE OF INVENTION: Phosphodiesterase
; FILE REFERENCE: 5800-28
; CURRENT APPLICATION NUMBER: US/09/330,970
; CURRENT FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: 09/277,423
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-330-970-34

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Query Match          65.0%; Score 13; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VLE 3
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Db      2 VLE 4

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Search completed: November 25, 2003, 14:08:57
Job time : 22 secs

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